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<b>(54) Title:</b> HUMAN NUCLEIC ACID FRAGMENTS, ISOLATED FROM BRAIN ADRENAL TISSUE, PLACENTA OR BONE MARROW  <b>(57) Abstract</b>  This invention provides a nucleic acid fragment encoding a gene product or portion thereof and comprising any one of: (a) a sequence selected from SEQ ID Nos 1 to 1193 from the attached sequence listings; (b) an allelic variation of a sequence as defined in (a); or (c) a sequence complementary to (a) or (b). The invention includes uses of such fragments, and gene products corresponding thereto.		

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# HUMAN NUCLEIC ACID FRAGMENTS, ISOLATED FROM BRAIN ADRENAL TISSUE, PLACENTA OR BONE MARROW

This invention relates to new nucleic acid fragments encoding gene products or portions thereof, which fragments are obtainable from human nucleic acid populations, individual members of such populations being present in widely varying amounts.

5 Situations are increasingly arising in which it is necessary to study complex nucleic acid or polynucleotide populations. For example, it is now widely appreciated that an invaluable resource could be created if the entire sequence of the genomes of organisms such as man were determined and the information available. The magnitude of such a task should not, however, be underestimated. Thus, the human genome may  
10 contain as many as 100,000 genes [a very substantial proportion of which may be expressed in the human brain (Sutcliffe, Ann. Rev. Neurosci. 11:157 (1988))]. Only a very small percentage of the stock of human genes has presently been explored, and this largely in a piecemeal and usually specifically targeted fashion.

15 There has been much public debate about the best means of approaching human genome sequencing. Brenner has argued (CIBA Foundation Symposium 149:6 (1990)) that efforts should be concentrated on cDNAs produced from reverse transcribed mRNAs rather than on genomic DNA. This is  
20 primarily because most useful genetic information resides in the fraction of the genome which corresponds to mRNA, and this fraction is a very small part of the total (5% or less). Moreover, techniques for generating cDNAs are also well known. On the other hand, even supposing near perfect recovery of cDNAs corresponding to all expressed  
25 mRNAs, some potentially useful information will be lost by the cDNA approach, including sequences responsible for control and regulation of genes. Nonetheless, the cDNA approach at least substantially reduces the inherent inefficiencies resulting from analysis of repeated sequences or non-coding sequences in an approach which depends upon  
30 genomic DNA sequencing.

Recently, the results of a rapid method for identifying and characterising new cDNAs has been reported (Adams, M.D. et al., Science  
35 252, 1991, pp 1651-1656). Essentially, a semi-automated sequence reader was used to produce a single read of sequence from one end of each of a number of cDNAs picked at random. It was shown, by comparing the nucleic acid sequences of the cDNAs (or the protein sequences produced by translating the nucleic acid sequence of the cDNAs) to each

other and to known sequences in public databases, that each of the cDNAs picked at random, could be unambiguously classified. The cDNAs could be classified as being either entirely new or as corresponding, to a greater or lesser extent, to a previously known sequence. cDNAs identified in this way were further characterised and found to be useful in a variety of standard applications, including physical mapping. Unfortunately, such a process is insufficient. The longer the process is pursued with any given population of cDNAs the less efficient it becomes and the lower the rate of identification of new clones. In essence, as the number of cDNAs which have already been picked rises, the probability of picking a particular cDNA more than once increases. This difficulty is exacerbated by the wide range of abundancies at which different cDNAs can occur, which abundancies can vary by several orders of magnitude. Thus, whereas some sequences are exceedingly rare, a single cDNA type may comprise as much as 10% of the population of cDNAs produced from a particular tissue (Lewin, B. Gene Expression, Vol. 2: Eukaryotic Chromosomes, 2nd ed., pp. 708-719. New York: Wiley, 1980). The need to avoid missing rarer species in any given population presents a considerable problem.

Various approaches (so-called "normalisation" techniques) have been tried in addressing the problem of increasing the efficiency of examination of a mixed nucleotide population, for example, such a population as is to be examined in human genome sequencing.

Thus, a standard PCR protocol can be used to amplify selectively cDNAs which are present at extremely low levels, if there is information about the sequence of those cDNAs. If not, a primer specific to the desired cDNA cannot be constructed and the desired cDNA cannot be selectively amplified. The standard PCR method is therefore inadequate if it is desired to characterise a number of unknown genes.

A second approach involves hybridization of cDNA to genomic DNA. At saturation, the cDNAs recovered from genomic/cDNA hybrids will be present in the same abundance as the genes encoding them. This will provide a much more homogenous population than the original cDNA library, but does not entirely solve the problem. In order to reach saturation in respect of the very rare sequences, it will be necessary to use huge quantities of cDNA, which need to be allowed to anneal to large amounts of genomic DNA over a considerable periods of time. Furthermore, cDNAs which are homologous to genes which are present in multiple copies in the genom will be over-represented.

A third approach exploits the second order reassociation kinetics of cDNA annealing to itself. After a long period of annealing, the cDNAs which remain single stranded will have nearly the same abundance, and can be recovered by standard PCR (see Patanjali, S.R. et al., PNAS USA 88, 1991, pp. 1943-1947; Ko, M.S.H., NAR 19, no.18, 1991, pp 5705-5711). The methods disclosed in these two publications, however, suffer from notable disadvantages. They are entirely dependent on the stringent physical separation of single stranded and double stranded DNA, require an elevated number of manual manipulations in each reaction, and necessitate protracted hybridisation times (up to 288 hours in the method of Patanjali et al.)

Yet a further approach in "normalising" a nucleotide population is described in co-pending British Patent Application No 91 15407.0, filed 17th July, 1991 by MRC, and involves a PCR process in which a mixture comprising a heterogenous DNA population and appropriate oligonucleotide primers is first formed and the DNA denatured, but before effecting a conventional PCR protocol the conditions are altered to allow the denatured strands of the more common DNA species to reanneal together, whilst avoiding annealing of primers to the DNA strands. By this means, rarer species can subsequently be amplified in preference to the more common species.

This PCR normalisation method in general comprises the steps of:

- (a) preparing a mixture comprising a heterogenous DNA population and oligonucleotide primers suitable for use in a PCR process, in which the DNA is denatured;
- (b) altering the conditions to allow the denatured strands of the more common DNA species to reanneal, while preventing the annealing to the primers to the DNA strands;
- (c) further altering the conditions of the mixture in order to allow the primers to anneal to the remaining single-stranded DNA comprising the rarer DNA species; and
- (d) carrying out an extension synthesis in the mixture produced in step (c).

Advantageously, the method consists of a cyclic application of the above four steps.

It will be appreciated that the conditions may be altered by the alteration of the temperature of the reaction mixture. However, any conditions which affect the hybridisation of complementary DNA strands to one another may be varied to achieve the required result.

5 Because the reannealing efficiency of any given DNA species will depend on the product of its concentration and time, the more abundant the sequence the greater the extent to which it will reanneal in any given time period. Once a DNA species has reached a certain threshold  
10 concentration it will no longer be amplified exponentially, as a significant amount will have annealed to the double stranded form before the priming step. Thus, as each individual DNA species is amplified by the process to its threshold concentration, the rate of amplification of that species will start to tail off. Eventually,  
15 therefore, all DNA species will be present at the same concentration.

The length of the reannealing step will determine how much DNA is present at the threshold concentration. Preferably, therefore, the duration of the reannealing step will be determined empirically for  
20 each DNA population.

In the PCR normalisation process in general, the DNA primers may be adapted to prime selectively a sample of the total DNA population. By using primers which will only prime a sample of the population, only  
25 that sample will be amplified and normalised. The total quantity of DNA generated will thereby be reduced, which means that the cycling times can be kept low. This ensures that the method is applicable to complex DNA populations such as cDNA populations. In addition, a first primer can be used which is adapted selectively to prime a sample of  
30 the total cDNA population, and a second primer which is a general primer. Advantageously, the general primer is oligo dT (each primed cDNA will then be replicated in its entirety, as the oligo dT primer will anneal to the poly-A tail at the end of the cDNA).

35 In co-pending British Patent Application No 92 14873.3, filed by MRC 13th July, 1992, a new process is described which allows the study and identification of the individual members of a mixed or heterogenous population of nucleotide sequences perhaps of varying abundance. In preferred embodiments of the said process, the starting nucleic acid  
40 population is treated by:

(a) subjecting the nucleic acid to the action of a reagent,

preferably an endonuclease which has its cleavage and recognition sites separated, which reagent cleaves the nucleic acid so as to produce double stranded cleavage products the individual strands of which overlap at cleaved ends to leave a single strand extending to a known extent;

(b) ligating the cleavage products from (a) with a population of adaptor molecules to generate adapted cleavage products, each of which adaptor molecules has a cleavage product end recognition sequence and the population thereof encompassing a range of adaptor molecules having recognition sequences complementary to a predetermined subset of the sequences of the cleavage-generated extending single strands; and

(c) selecting and separating only those adapted cleavage products resulting from (b) which carry an adaptor of predetermined recognition sequence.

A preferred endonuclease for use in step (a) of the above process is Fok I.

An important feature of this process is the use of adaptor molecules. The adaptors used must have "overhanging" fragment recognition sequences which reflect or are complementary to the extending cleavage-derived sequences which the adaptors are designed to react with. It is also preferred that the adaptors used should end with a 5' hydroxyl group. The avoidance of a 5' phosphate group removes the risk of inappropriate ligation involving the adaptors.

Adaptor molecules may also contain a portion permitting specific sequence selection and separation (as in step (c) of the process) when a sequence is attached to the adaptor. For example, an adaptor can carry biotin, thereby permitting advantage to be taken of the biotin/avidin reaction in selecting and separating desired adapted molecules. Additionally, adaptors preferably comprise a known and selected sequence such that specifically isolated adapted molecules can be amplified by known techniques (such as PCR) using a primer complementary to the core sequence.

Preferably the adaptors are short double-stranded oligonucleotides which can be joined to the ends of cleavage products. They will have been chemically synthesised so that their sequence can be predetermined

and so that large concentrations can be easily produced. They may also be chemically modified in a way which allows them to be easily purified during the process. As mentioned above, ideally their 5' ends will be unphosphorylated so that once joined to fragments the adapted end of the latter will no longer be able to participate in further ligation reactions.

It is preferred that the adaptor cleavage product end recognition sequences are on the 5' end of the longest oligonucleotide strand making up the preferred adaptor molecules, are at least 3 nucleotides in length and with totally random bases at the single-stranded position(s) two nucleotides in from the 5' end. This then allows selection to be performed both during the joining reaction and during subsequent priming reactions. Then, because the final degree of selection is a result of the product of the degrees of selection achieved at these two stages, maximum selection can be achieved per adaptor/primer available.

Adaptor strand extensions on the 5' end of the longest oligonucleotide also facilitate the use of modified oligonucleotides for separation purposes. Preferably, the short oligonucleotide will be modified at its 5' end. This has the double benefit of requiring just one modified oligonucleotide for all possible single-stranded extensions that are used, and also placing the modification at a position where it cannot interfere with ligation or subsequent priming reactions.

Although only one type of adaptor is required per ligation reaction, it is preferred that adaptors covering all possible reactions in a chosen subset of sequences be present, because then the opportunity for fragments in the chosen subset to ligate to each other is minimised. It is also preferred that the chosen specific adaptor, carrying a predetermined recognition sequence, should not only be different from the other adaptors in its single-stranded extension, but also different in the rest of its sequence since this allows orientation to be introduced which is useful in subsequent steps. It is therefore also preferred that this adaptor has a modified oligonucleotide to facilitate its separation with the cleaving products to which it joins.

The above "adapting" process can be used to generate categories or subsets of sequences by making some of the adaptors specific in some way, and selecting and separating as in step (c). In this way subsets of sequences can be provided depending upon the specific adaptor

chosen, e.g. for use in subsequent nucleotide sequencing. This facilitates, for example, the identification of a large population of sequences by permitting a rational approach to splitting such populations into subsets, each of which subsets can be examined in turn.

In the light of these developments, the present invention now provides a nucleic acid fragment encoding a gene product or portion thereof and comprising any one of:-

- (a) a sequence selected from SEQ ID Nos 1 to 1193;
- (b) an allelic variation of a sequence as defined in (a); or
- (c) a sequence complementary to (a) or (b).

In another aspect, the invention provides a nucleic acid sequence as set out in any one of SEQ ID Nos 1 to 1193, or a complement or allelic variation thereof. Preferred sequences exhibit no more than 90% homology to a human sequence known per se.

In a further aspect, the invention provides a nucleic acid fragment comprising a portion of a sequence as defined above of sufficient size such that a probe of the same size and exhibiting complementarity to said portion can hybridise to said sequence. Preferably, such portions are at least 15 bases in length. It will be appreciated that minor mismatches in the aforesaid "complementarity" are not excluded provided hybridisation can still occur. In general, hybridisation conditions are within the choice of the skilled person, but reference can be made, for example, to the following: Melting temperature of hybrids - Bolton, E. T. and McCarthy, B. J. Proc. Natl. Acad. Sci, 48 p1390 (1962). Effect of formamide on lowering melting temperature - Casey, J. and Davidson, N., Nucleic Acids Res. 4, p1539 (1977). Effect of imperfect homology - Bonner, T. I. et al., J. Mol. Biol. 81, p123 (1973). General - Meinkoth, J. and Wahl, G. Anal. Biochem. 138, p267 (1984). Oligo hybridization and washing - Lathe, R. J. Mol. Biol. 183, P1 (1985).

The present invention also envisages DNA constructs comprising fragments or sequences as referred to above with a control or regulatory sequence.

The invention includes such DNA constructs using a gene system known in the art ligated to a sequence or fragment of the invention so as to enable, upon expression, the provision of a fusion polypeptide. Preferably, an endopeptidase recognition site is provided such that  
5 when the sequence or fragment is expressed it is expressed in frame with a known protein with the boundary being a cleavage site for an endopeptidase with a rare cutting site. The known protein can then be affinity purified, and the peptide corresponding to the fragment or  
10 sequence in accordance with the invention may be released by the endopeptidase. Alternatively, the whole protein can be used to raise antibodies which can then be screened for those directed at polypeptide corresponding to the fragment or sequence of the invention.

15 Since the present fragments and sequences can be used to produce, inter alia, corresponding genes, whether by isolating them, by synthesis or otherwise, such use and the resulting DNA fragments comprising genes are further aspects of the invention.

20 Yet another aspect of the invention is an expression vector comprising a fragment, sequence, gene-comprising DNA fragment, or DNA construct, as above, positioned such that that nucleic acid sequence which encodes the polypeptide corresponding to said fragment, sequence or DNA fragment is in operable reading frame with a control or regulatory  
25 sequence.

Other aspects of the invention are host cells incorporating a sequence, or fragment, or gene-comprising DNA fragment, or DNA construct, as above, as a heterologous part of the expressible genetic information of the cell. The production of such modified host cells can be achieved  
30 using methods known in the art. Such modified host cells can be used to express corresponding proteins, and these materials lend themselves in turn to the preparation of corresponding monoclonal or polyclonal antibodies using standard techniques.

35 Also included in this invention are such antibodies. Reference can be made, inter alia, to the following literature: Monoclonal antibodies, Cambell, A. M. Laboratory Techniques in Biochemistry, and Molecular Biology Ed. Burdon, R. H. and van Knippenberg, P. H. vol 13. Elsevier Amsterdam 1984. Goding, J. W., Monoclonal antibodies: Principles and  
40 Practice, 2nd Edition, academic Press, London 1986. Kipps, T. J. and Herzenberg, L. A., Handbook of Experimental Immunology : Applications of immunological methods in biomedical sciences, 4th edition Ed. Weir,

D. M. t al., p108 Blackwell scientific Publications, Oxford. Harlow, E and Lane, D. Antibodies, A Laboratory Manual, Cold spring harbor Laboratory, Cold Spring, New York.

5 Expression in an appropriate higher eucaryotic host may be important to ensure correct protein folding and also activity. Expression to avoid copurification of toxic products can sometimes be better performed in organisms approved for human consumption, eg prokaryotic *Bacillus subtilis*, eukaryotic yeast, mammalian cows milk vectors, and other  
10 methods known in the art.

The invention also includes novel gene products or portions thereof encoded by a fragment, sequence or gene-comprising DNA fragment of the invention.

15 It will be appreciated that the sequences of the present invention collectively have utility based, inter alia, upon their common origin, and hence they can effectively be considered together rather than as separate entities. It is convenient to represent them as separate  
20 sequences, because this is how they were produced and serves as "punctuation" between the different functional entities which each sequence represents. However, the sequences could just as easily have been presented as a continuous sequence derived by placing them end to end in the order in which they were produced, with a separate  
25 indication of where the beginnings and ends of the component sequences are.

In contrast to investigations hitherto, where gene fragments (sequence fragments) could only be identified through some known characteristic  
30 [for example: their homology to a fragment which largely encodes amino acids identified by sequencing a previously isolated peptide or is the antisense of that coding sequence; or them having at least partial homology to previously characterised nucleic acids; or them having ability to encode expressed proteins which could later be detected by  
35 functional assays of the cells expressing those proteins or by using antibodies which had been previously raised against the proteins to detect their expression, Sambrook J., et al., Molecular Cloning CSH Press 1989], the sequences and fragments described by the present invention are entirely underivable and unpredictable from the prior  
40 art, but are nonetheless clearly of great value for various purposes.

Thus, such sequences, by comparing them to sequence databases, can be

used as a means for determining the existence of new members of existing gene families, new human genes when previously only non-human genes were known and new genes when previously no genes were known (Karlin, S. and Altschul, S. F. Proc. Natl. Acad. Sci. 87 p2264-2268 (1980)). In all cases, this allows the isolation of the corresponding genes and their products, and hence enables the manufacture of molecules of potential biological interest by recombinant means. Screening libraries of known materials or hitherto unexplored source materials for biological efficacy is now an important industrial activity in the search for new therapies and therapeutics. When new sequences have already been found to have counterparts in gene families or in non-human genes then knowledge about biological efficacy may already be apparent. For example, new receptors or receptor agonists/antagonists may exhibit differences to known instances of these molecules, and such differences could make them more suitable as therapeutics by, for example, exhibiting binding characteristics which are more in keeping with avoidance of toxicity. Reference can be made, for example, to polymorphic dopamine receptors and the implications for mental health (Iversen, L. Nature 358, p109 (1992), and Van Tol, H. M. M. et al., Nature 358, p149-152 (1992)). Where absolutely required, realisation of full length cDNAs for expression can be achieved by using the sequences to screen (by hybridisation) suitable cDNA libraries containing full length clones (D'Alession, J. M., et al., Focus (Gibco B.R.L) 9 pl (1987)). Alternatively, the sequences can be used to design primers suitable for obtaining the missing sequences by PCR or other amplification methods (Frohman, M. A., Dush, M. K. and Martin, G. R., Proc. Natl. Acad. Sci. 85 p8998-9002 (1988)).

Appropriate use of the sequence fragments in antisense or triple helix (Griffin et al., Science 245 p967-971 (1989)) applications will be useful for identifying manipulable targets related to disease. For example, viruses have been inhibited by antisense RNA to their mRNAs (Chang, L-J., and Stoltzfus, C. M. J. Virol. p921-974 (1987)). A similar effect could be achieved by targetting the expression of cellular proteins which are essential for growth or maintenance of the virus.

Partial or full length cDNAs have great utility once expressed. The manner of expression can be selected by one skilled in the art to suit the intended application. Expression of full length cDNAs is typically required for biological activity. Prokaryotic, and lower or higher eucaryotic hosts may be selected as the host for expression and higher

eucaryotes may be preferred to ensure correct modifications, for example, glycosylation in vivo, when this proves to be important. Expression can be ensured by situating the cDNA appropriately to signals for expression (Amann, E. and Brosius, J. *Gene* 40 p183 1985), Shimuzu, Y et al., *Gene* 65, p141 (1988), Straus, D. and Gilbert, W. *Proc. Natl. Acad. Sci.* 82, p2014 (1985)). Such signals may include a promoter for transcription, which may itself be regulatable.

The proteins thus-expressed can be screened for activities of therapeutic or commercial value. It may be that the proteins have to be first isolated for this purpose or can be assayed in situ. It may be desirable that some means of stabilising the expressed protein is employed. This can be achieved, for example, (and as indicated earlier) by expressing in frame as part of a fusion polypeptide (Smith, D. B., et al., *Proc. Natl. Acad. Sci.* 83 p8073 (1986)).

Useful antibodies can be raised against the expressed proteins. It is commonly not an absolute requirement that full length proteins are produced, although this may influence the quality of the antibodies produced. Peptides as short as 8 or 9 amino-acids in length can be used as antigens (Germain R., N. *Nature* 353 pp605-607 (1991), Rudensky, A., Y., et al., *Nature* 353 p622-627 (1991)). Immunogenic peptides could simply be synthesised using the amino-acid sequence translated from a sequence or fragment of this invention. It is desirable, although not absolutely required, that some means of producing purified antibodies is adopted. When fusion polypeptides are used to raise antibodies, an affinity matrix specific for the generic part of the protein allows the fusion polypeptide to be immobilised (Smith, D. B., et al., *Proc. Natl. Acad. Sci.* 83 p8073 (1986)). The immobilised polypeptide can then be used to affinity purify the antibodies. Antibodies to both the generic part of the fusion polypeptide and the part of interest are produced. When these need to be discriminated between, a different affinity column can be used to remove only those antibodies specific for the generic part of the polypeptide. Alternatively, and as mentioned earlier, it can be arranged that the boundary between the two separate protein components of the fusion polypeptide has the recognition sequence for an endopeptidase with a rare cutting site. The peptide of interest can then be released from the affinity purified polypeptide by the action of the endopeptidase (Nagai, K., and Thogersen, H., *C. Methods Enzymol.* 153 p461-481 (1987)). Another alternative is raise monoclonal antibodies against the purified protein.

The antibodies can be used for localising in situ, or quantifying in samples through, for example, ELISA or RIA assays, peptides against which they were raised. These uses are particularly beneficial when the results of the assays can be correlated to a disease condition, eg cancer. For example tumour markers may be found and used to target therapeutic agents. The antibodies can also be used to detect or monitor markers of undifferentiated growth, infection, cardiovascular or immune disease or a therapeutic response. When the antibodies recognise cell surface proteins they can be used in isolation or in combination to isolate particular populations of cells. These in turn can be used to isolate yet more cDNAs which will be enriched for yet more of such surface markers for the population, which, if similarly screened, will permit yet further subdivision of the population. Ultimately, panels of antibodies which can describe particular disease states will accrue. Such antibodies could be tailored for forensic applications as well as diagnostic purposes and disease monitoring.

The sequences or fragments can also be used for genetic analysis and mapping, for example, to diagnose the likelihood that a given individual is predisposed towards a given genetic disease. In the event of a sequence co-locating, genetically, with a disease gene, it can be used for the derivation of new disease therapies bases upon precise genetic knowledge. Such therapies can include, for example, the techniques of so-called "gene therapy" (Dusty Miller, A. Nature 357 p455-460 (1992)).

Antibodies can be produced against the protein of a genetic disease with sufficient discriminating power to discriminate between diseased and non-diseased states (Caskey, T. Genome Sequencing Conference, Hilton Head, S. Carolina (1991)). This would be useful for reducing the dependence of such tests on nucleic acid-based screens. Such antibodies also have the advantage of allowing detection of faulty expression of the protein, for example levels of expression which may be important for development of the disease in slow onset conditions.

Also very important is that not all cDNAs are likely to be found by conventional means, whereas the present sequences are, in one sense, "comprehensive". The use of the class of cDNAs which corresponds of necessity to truncated clones increases the chances that part of a cDNA will be cloned free of any sequences that could otherwise compromise it from being cloned. Sequence obtained can then be used to generate PCR primers from which the remainder can be obtained without having to

clone.

This invention will now be further described and illustrated by means of the following Examples.

5

All oligonucleotides used in these Examples were synthesised Trityl on using an ABI 380B DNA Synthesizer according to the manufacturers instructions. Purification was by reverse phase HPLC (see, for example, Becker, C., R., et al., J. Chromatography 326, p293-299 (1985)).

10

#### Example 1

Human brain and adrenal tissues were obtained from a mixture of 12 to 15 week menstrual age fetuses and then snap frozen in liquid nitrogen before storing in bijoux bottles in a -80°C freezer. The two types of tissue were used separately, directly from the freezer, to prepare cDNA from which restriction fragments were generated for sorting into subsets. 1g portions of each of the separate tissues were homogenised, using an Ultra-Turrax T25 Disperser (Janke and Kunkel, IKA-Labortechnik), on ice in the presence of 4M guanidinium isothiocyanate to solubilise macromolecules. RNA was isolated from each homogenate by using centrifugation to sediment it through caesium trifluoroacetate. This was performed using the Pharmacia kit according to the manufacturer's instructions, except that centrifugation was performed for 36 hours and the RNA obtained was finally desalted and concentrated by performing two ethanol precipitations in succession with two 70% ethanol washes after each precipitation. In each case, polyA<sup>+</sup> (mRNA) was isolated from 200 to 400 µg of the total RNA by binding it to magnetic oligo-dT coated beads (Dynal). Solution containing unbound material was removed from the beads, which were washed, and then mRNA eluted directly for use. mRNA isolation was performed in accordance with the manufacturer's instructions. Yields of RNA from the beads were between 1 and 3% of the total RNA. 2 to 4 µg of the eluted RNA were used for cDNA synthesis. cDNA synthesis was performed according to the method of Gubler, U and Hoffman, (B. J. Gene 25 p263 (1983)) using a Pharmacia kit according to the manufacturer's instructions. OligodT was used to prime the first strand cDNA synthesis reaction. The cDNA was purified by extracting twice with phenol/chloroform and then low molecular weight solutes including nucleic acids below ca. 300 bases were removed by passing the cDNA reaction mixture through a Pharmacia S400 spun column used according to the manufacturer's

40

instructions. Running buffer for the column comprised 10 mM TrisHCl, 1 mM EDTA, 50 mM NaCl @ pH 7.5.

5 The column eluate was adjusted to 10 mM  $Mg^{2+}$  and then the purified cDNA was restricted by the action of 1 unit per 10  $\mu$ l of the endonuclease Fok I at 37°C for 1 hour, so that it would be able to accept adaptors to enable fragment sorting.

10 The cDNA fragments were purified by two successive phenol/chloroform extractions followed by passing them through S400 spun columns as described above.

The adaptors used were oligonucleotides 5'  $N_4N_4N_4N_4TCCTTCTCCTGCGACAGACA$  (SEQ ID: 1194) with the complementary strand 5'  $TGTCTGTGCGAGGAGAAGGA$  (SEQ ID: 1195) and 5'  $AAN_4N_4TCTCGGACAGTGCTCCGAGAAC$  (SEQ ID: 1196) or 5'  $TTN_4N_4TCTCGGACAGTGCTCCGAGAAC$  (SEQ ID: 1197) each with the complementary 5' biotinylated strand  $GTTCTCGGAGCACTGTCCGAGA$  (SEQ ID: 1198). These were added to 25% of the eluted material by incubating together 200 pmoles of the mixture of double-stranded adaptors in the elution buffer to which had been added  $MgCl_2$  to 10mM, ATP to 10mM and 0.025 units/ $\mu$ l of T4 DNA ligase. The oligonucleotide 5' biotinylated  $GTTCTCGGAGCACTGTCCGAGA$ , (SEQ ID: 1198) and whichever of the complementary oligonucleotides with which it was used, each comprised 1/32 of the molar proportion total adaptors. The final reaction volume was 90  $\mu$ l which was heated to 65°C for 3 minutes and then cooled to room temperature before the ligase was added. Ligation was performed for 16 hours at 12°C.

30 Two successive phenol/chloroform extractions were performed to remove the ligase. The final aqueous phase was passed through an S400 spun column (Pharmacia) as described above except that the column was used with 10 mM Tris pH 8.3/50 mM NaCl.

35 The column eluate was adjusted to 25mM  $Mg^{2+}$ , 0.5mM dNTPs in a final volume of 200  $\mu$ l. The mixture was placed in a thermocycler (Techne MW2) and heated to 78°C for 5 minutes. At this point 10 units of cloned Taq DNA polymerase (AmpliTaq, Perkin Elmer) were added. This was followed by an incubation at 72°C for 10 minutes to fill in the unligated strand of the adaptor. After the second incubation 200  $\mu$ l of streptavidin coated magnetic beads (Dynal) prepared according to the manufacturers instructions were added to bind cDNA ligated to that of the oligonucleotides which was complementary to the 5'

GTTCTCGGAGCACTGTCCGAGA (SEQ ID: 1198) biotinylated adaptor. Bead binding was allowed to proceed at 28°C for 30 minutes with mixing every 10 minutes.

5 Un-biotinylated cDNAs were washed from the beads with 400µl each of 2M NaCl twice, fresh 0.15 mM NaOH four times at 28°C for 5 minutes each, water twice and finally a buffer comprising 20 mM Tris pH 8.3, 50 mM NaCl, and 25mM Mg<sup>2+</sup>. The beads were then resuspended in 240 µl of the  
10 final buffer including additionally 0.5 mM dNTPs and divided into 4x60 µl.

Four of the 60 µl aliquots, two from each tissue, were processed further specifically to prime and copy a subset of the immobilised, adapted fragments. 2 pmoles of the primer 5' CTGTCTGTCGCAGGAGAAGGAA  
15 (SEQ ID: 1201) were added to each of two aliquots, one from each tissue. 2 pmoles of the primer 5' CTGTCTGTCGCAGGAGAAGGAG (SEQ ID: 1202) were added to each of the other two aliquots. 2.5 units of Taq DNA polymerase were added to each reaction and 16 cycles of alternate denaturation at 95°C for 30 seconds, annealing at 63°C for 2 minutes  
20 and polymerisation at 72°C for 3 minutes was performed to accumulate the selected single-strands in solution.

On completion of the DNA synthesis reactions a further 30 µl of resuspended beads were added to each reaction to remove the  
25 biotinylated fragments. The reaction was incubated at 28°C for 30 minutes mixing every 10 minutes to ensure that the biotinylated strands were bead bound. Each aqueous phase containing the newly synthesised strands was then removed and extracted with phenol/chloroform twice to remove the enzyme before being further purified by passing through an  
30 S400 spun column equilibrated with 10 mM Tris pH 8.3/50 mM NaCl as described above.

Rounds of PCR amplification of subsets of the selected fragments were performed by using the original primer in each case, together with one  
35 of the primers 5' GTTCTCGGAGCACTGTCCGAGAG (SEQ ID: 1199) or 5' GTTCTCGGAGCACTGTCCGAGAC (SEQ ID: 1200). This simultaneously rendered the fragments double-stranded and increased the amounts of available material. It was not known how many cycles of amplification would be required at this stage, since each primer pair would be expected to  
40 behave differently. It was therefore necessary directly to determine a suitable number empirically by using standard agarose gel electrophoresis to examine the reaction products after a given number

of cycles. In some cases, to avoid the accumulation of non-specific products, it was necessary to perform an initial 5 cycles of amplification with both of the primers present at 2 pmoles each. All reactions were performed using 8  $\mu$ l or 12.5 % whichever was the larger but not exceeding 12  $\mu$ l of the column effluent above. Reaction conditions were adjusted to 20 mM Tris pH 8.3, 50 mM NaCl, 25mM  $Mg^{2+}$ , 0.5mM dNTPs and 2.5 units of Taq DNA polymerase in a final volume of 40  $\mu$ l. Apart from when an initial amplification with 2 pmoles of each primer was performed, 20 pmoles of each primer were used. Cycles of amplification were performed at 95°C for 30 seconds, 65°C for 1 minute and 72°C for 3 minutes.

For the purposes of cloning, selected cDNA was amplified as described immediately above, except that the reaction was not monitored. Instead, the number of cycles which had previously been shown to just give rise to all observable products plus another 4 cycles were performed. In addition, an extra 72°C for 10 minutes incubation was performed after the last cycle.

The products of the reaction were then prepared for directional cloning. Water was added to adjust the final reaction volume to 60  $\mu$ l. Enzyme was removed by two successive phenol/chloroform extractions. The final aqueous mixture was passed through an S400 column as described above, except that it had been equilibrated with 10 mM Tris HCl pH 7.5, 50mM NaCl.

For directional cloning, advantage was taken of the different known sequences introduced at each end of the selected cDNAs by the adaptors in a modification of the method of Aslandis, C. and de Jong, P. J. (Nucl. Acids Res. 18, p6156 (1990)). Different cohesive ends were produced on each end by using the exonuclease activity of T4 DNA polymerase to resect from the 3' end, to the first T in each case. To 75  $\mu$ l or 75 % of the column eluate, whichever was least, were added 9.5  $\mu$ l of 100mM TrisHCl pH7.4, 100 mM  $MgCl_2$ , and 9.5  $\mu$ l of 0.5 mM dTTP. 16 units of T4 DNA polymerase were added and the reaction incubated in a water bath at 37°C for 30 minutes. The enzyme was removed by extracting with phenol/chloroform, twice successively. The salt of the final aqueous phase was adjusted by passing it through an S300 column (Pharmacia) equilibrated with 10 mM TrisHCl pH 7.4, 1 mM EDTA as described above.

The E.coli plasmid cloning vector pBluescript KS+ (Alting-Meese, M. A.

and Short J. M., Nucl. Acids Res. 17 p9494) was prepared for accepting the resected cDNA by restriction cleavage at the BamHI and HindIII sites and then adaptoring the resultant cohesive ends using the specific adaptors produced by the oligonucleotide 5' AGCTCGGCTCGAGTCTG (SEQ ID: 1203) with its partially complementary oligonucleotide 5' GCGACAGACAGCAGACTCGAGCCG (SEQ ID: 1204) and the oligonucleotide 5' GATCCGGCTCGAGT (SEQ ID: 1205) with its partially complementary oligonucleotide 5' CCGAGAACACTCGAGCCG (SEQ ID: 1206). Preparation of the vector and adaptoring were performed according to standard procedures. Insertion of the cDNA was performed between the BamHI and HindIII restriction sites. Recombinant vectors were transformed into the host XL1-Blue (Bullock, W. O. et al Biotechniques 5 p376-378 (1987)) by the method of Hannahan, D. J. (Mol. Biol. 166 p577-580 (1983)). Suitable standard controls for the ligations and transformations were also included.

Post transformation procedures were as described in "Molecular Cloning", 2nd Edition (Sambrook J., Fritsch, E. F., and Maniatis, T. CSH Press (1989)). Colonies were produced by plating onto X-gal/IPTG L-agar plates containing 50µg/ml ampicillin and 10µg/ml tetracyclin. Clear colonies were picked, each into a separate well of a microtitre plate, containing 100µl of L-broth and 50µg/ml ampicillin. Growth was allowed to occur for 16 hours at 37°C. 100µl of 50% or 30% glycerol was added to plates which were archived at -20°C or -80°C, respectively.

Bacteria corresponding to those archived were used for preparing templates for sequencing by the dideoxy method (Sanger, F. Milklen, S. and Coulson, A. R. Proc. Natl. Acad. Sci. 74 p5463-5467 (1977)). Bacteria for this purpose were either grown on L-agar plates containing 50µg/ml of ampicillin, prepared at the same time as they had been grown in liquid culture, or after plating out from the archive. Alternatively, fresh liquid cultures were inoculated from the archive.

In all cases, cDNA inserts were amplified for sequencing by PCR (Saiki, R. K. et al Science 239 p487-491 (1988)). PCR was either performed using bacteria directly added to the reaction, by a toothpick, or PCR was performed using 1/50th of the plasmid isolated by preparative methods (Holmes, D. S. and Quigley, M. Anal. Biochem. 114 p193 (1981)) from the bacteria in the liquid cultures or from the plates.

20 pmoles of each of the PCR primers 5' biotinylated GTAAAACGACGGCCAGT

(SEQ ID: 1207) and 5' CGAGGTCGACGGTATCG (SEQ ID: 1208) were used in 40µl reactions containing 2.5mM Mg<sup>2+</sup>, 50 mM KCl, Tris-HCl pH 8.3 and 0.25 units of Amplitaq (Cetus). Reactions were performed at 95°C, for 1 minute, followed by 35 cycles at 95°C for 30 seconds, 60°C for 30 seconds and 72°C for 40 seconds. After the cycles, a final incubation at 72°C for 5 minutes was performed.

After PCR, standard agarose gel electrophoresis was used to determine which reactions had been successful. The biotinylated strands of successful reactions were then recovered for single-stranded sequencing by binding them to streptavidin coated beads (Dynal) and then washing, all according to the manufacturers instructions, except that the washing steps were either performed manually or performed automatically in the 96 well microtitre plate format using a Biomek robotic work-station attached to a side-arm loader (Beckman).

Dideoxy chain termination sequencing reactions were performed using the immobilised, biotinylated strands as templates and 2 pmoles of the oligonucleotide 5' CGAGGTCGACGGTATCG (SEQ ID: 1209) as primer. Reactions were performed using fluorescently-labelled terminators (Du Pont) or a fluoroscein-labelled primer (Pharmacia) according to the manufacturers instructions. Reactions were analysed using automated DNA sequencers. A Genesis 2000 was used for the "Du Pont" reactions and an A.L.F. for the "Pharmacia" reactions. Bases were assigned for the Genesis 2000 reads using the manufacturers Base Caller software. Files of called bases were then transferred to a SUN Network from an Apple Macintosh computer which had been used for base calling. Raw data from the A.L.F. reads was directly transferred to a SUN network where bases were called using the public domain "trace editor software" (TED). In both cases, files of called bases were entered into a Sybase™ database. Entering data entailed automatically removing vector and adaptor or linker sequences, but not editing ambiguous bases. After removal of the unwanted bases, files were automatically compared to other sequences in the cDNA database and the latest versions of the publically available databases, GENBANK and SWISSPROT. Searches were performed with the "basic local alignment search tool" (BLAST) (Karlin, S. and Altschul, S. F. Proc. Natl. Acad. Sci. 87 p2264-2268 (1990)).

Sequences SEQ ID Nos 1 to 610, given hereinafter, were obtained by the above procedure.

#### Example 2

A second method of preparing cDNA libraries for obtaining gene fragments of the invention took advantage of the PCR normalisation process described above. Standard procedures were used to prepare mRNA from RNA that had been isolated by standard caesium chloride bouyant density gradient methods from a full term human placenta. The oligonucleotide LNotdt, sequence 5' TACGTTGACAAGCTTGAATTCGCGGCCGC(T)<sub>26</sub>, (SEQ ID: 1210) was used at 1  $\mu$ M with AMV reverse transcriptase, to prime first strand cDNA synthesis under standard conditions from 0.5  $\mu$ g of the placental mRNA. Temperatures above 65°C were used to inactivate the reverse transcriptase and then the volume of the reaction made up to 100  $\mu$ l with water.

PCRs were then performed in reactions containing 1  $\mu$ l of the diluted cDNA, 10 mM Tris-HCl pH 8.3, 40 mM KCl, 1.5 mM MgCl<sub>2</sub>, 0.01% gelatin, 200  $\mu$ M dNTPs, 10 uCi a<sup>32</sup>P dCTP, 1  $\mu$ M each of the primers 11AD1, sequence 5' GCC(TA)(GC)CGCCGA (SEQ ID: 1211), and LNotdT and Taq DNA polymerase. An initial denaturation period of 95°C for 90 seconds was followed either by 35 cycles of standard PCR, comprising 95°C for 30 seconds, 45°C for 30 seconds and 72°C for 30 seconds or alternatively 3 cycles of the standard PCR already described followed by 27 cycles of C<sub>ot</sub> PCR during which an additional step of 72°C for 16 minutes was placed between all of the 95°C and 45°C steps of the standard PCR. The standard PCR was followed by a single 72°C for 3 minutes step while the C<sub>ot</sub> PCR was followed by one standard PCR cycle except that the 72°C incubation was performed for 3 minutes.

Products of the PCR reaction were end repaired by adding 5 units of T4 DNA polymerase to the reaction and then incubating at 37°C for 10 minutes. Enzymes were removed by phenol extraction. The cDNA was precipitated by 70% ethanol, dried and then resuspended in NotI buff r. 20 units of NotI were used to digest the cDNA under standard conditions. cDNA was again phenol extracted and ethanol precipitated. 10% of the purified NotI cut DNA were ligated to the vector pBluescript lting-Meese, M. A. and Short J. M. Nucl. Acid Res. 17 p9494 which had been prepared as standard to receive this DNA by restricting with the enzymes NotI and EcoRV. Transformation and processing of clear colonies was performed as described above except that the host E.coli strain DH5a was used in place of XL-1 Blue.

Preparation of clones for sequencing, sequencing and sequence analysis of cDNAs in clones thus-produced were performed as described in Example 1.

Sequences SEQ ID Nos 611 to 772, given hereinafter, were obtained by the above procedure.

### Example 3

5

cDNA libraries corresponding to adult brain cortex (Clontech Laboratories, Inc., Cat No. HL10036) and adult bone marrow (Clontech Laboratories, Inc., Cat No. HL10586) prepared in lambda gt11 phage were transfected into E.coli Y1090 and plated out for colour selection of recombinant plaques ("Molecular Cloning", 2nd Edition Sambrook J., Fritsch, E. F., and Maniatis, T. CSH Press (1989)). 192 lambda Zap clones, corresponding to rhabdomyosarcoma cDNAs and a gift from C. Cooper, ICR, Sutton, were similarly plated except that the host XL-1 Blue was used.

15

Clear plaques from each library were resuspended in 5  $\mu$ l of Tris-HCl pH 8, 1 mM EDTA. 2  $\mu$ l of the resultant phage suspensions were added directly to PCRs for the purpose of amplifying the cDNA inserts for sequencing. PCR was performed as described in Example 1, except that the oligonucleotides used as primers for the lambda gt11 clones were 5' GGTGGCGACGACTCCTGGAGCCCG (SEQ ID: 1212) and 5' TTGACACCAGACCAACTGGTAATG (SEQ ID: 1213). Whichever of the oligonucleotides was to be used to prime the strand which would serve as the sequencing template was used in biotinylated form.

25

Preparation of clones for sequencing, sequencing and sequence analysis of cDNAs in clones thus-produced was performed as described in Example 1, except that 2 pmoles of the primers that were unbiotinylated in the PCR were used as sequencing primers.

30

Sequences SEQ ID Nos 773 to 1193, given hereinafter, were obtained by the above procedure.

The following are the SEQUENCE LISTINGS which comprise sequences SEQ ID Nos 1 to 1213 referred to hereinbefore. Certain of these sequences are preferred, and are listed as such after the main SEQUENCE LISTINGS.

35

21

## (1) GENERAL INFORMATION

## (i) APPLICANT

(A) NAME: MEDICAL RESEARCH COUNCIL

5 (B) STREET: 20 PARK CRESCENT

(C) CITY: LONDON

(E) COUNTRY: ENGLAND

(F) POSTAL CODE: W1N 4AL

10 (ii) TITLE OF INVENTION: HUMAN GENOME SEQUENCES

(iii) NUMBER OF SEQUENCES: 1213

(iv) COMPUTER READABLE FORM:

15

(A) MEDIUM TYPE: DISKETTE

(B) COMPUTER: IBM PC COMPATIBLE

(C) OPERATING SYSTEM: MS-DOS

(D) SOFTWARE: EXTRACT

20

(2) INFORMATION FOR SEQ ID :1:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 264 base pairs

25 (B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1:

GCCGATTCGT GACCAAGAAG GCTCTGTGCA TTCGGGTTTT CCAGGAGACT 50

35 CAAAAGCTGA AGAAGCGAAG AAGAGCCTTA AAGGCTGCAG CAGCAGCTCA 100

ATAACAAGC AAAGCGGAGG AACCCAGACA GCCCTTGTCC AAAGCCATAC 150

CAATATGATC TATCTTCTAA TGTATCCATG TTGTAATTAT ATATGTGTCT 200

40

GTGTGTGTCG AAATCTCTAG ACATACAGAT ATATATTCAT ATATCATATA 250

22

TATATATATA CACA

264

## (2) INFORMATION FOR SEQ ID :2:

5

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :2:

15

AGGAACATGT GTTTATTCAT CCAGCAGTGT TGCTCAGCTC CTACCTCTGT

50

GCCAGGGCAG CATTTTCATA TCCAAGATCA ATTCCCTCTC TCAGCACAGC

100

CTGGGGAGGG GGTCAATTGTT CTCT

124

20

## (2) INFORMATION FOR SEQ ID :3:

25

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 333 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :3:

ACAGAGCCGA TTCTGCATCC ACTGTGGTCA ACATTTAGGA AGTTTTAAGC

50

35

TAAGATTTGC CAAATTGTAG CCTACTGGAT TCCGGTTCTC TTGACATCTC

100

TTTCTAGTAG CCATGTCTTG CACTTCCCGA GTATAAACGA ACTGAGATGC

150

AAATTAAAAA AGGGAGGATT TAGAATAATG AAAAGAGAAA AGTCAAGAAA

200

40

GCACAATCAC TAGTGTAGAG ATAACAGAAT TTCTGAATTC CCTGAAAGCA

250

ATCTATATAA ATGCATGTGA AATAATACAC CAGCATCTGT GGCCCATACG 300

TCACATATTA GGAAGTATA ACATAAGGTA AAC 333

5 (2) INFORMATION FOR SEQ ID :4:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 200 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :4:

AGGGAGAAAG GAACATCCGC GAACAGCCAA AGAAATCTCA GAAGAGTCCC 50

GGAGCTCAAG GATCAGAGTA ACACAATTTT CACTTTTTCT GTCTTTATGT 100

20 AAGAAGAAAC TGCCTAGATG ACGGGGCCTC CTTCTTCAAA CAGGAATTTC 150

TGTTAGCAAT ATGTTAGCAA GAGAGGGCAC TCCCAGGCCC CTGCCCCCAT 200

25 (2) INFORMATION FOR SEQ ID :5:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 213 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :5:

ACAGAGCCAT TTGCATCCAC TGTGGTCAAC ATTTAGGAAG TTTTAAGCTA 50

AGATTTGCCA AATTGTAGCC TACTGGATTC CGGTTCTCTT GACATCTCTT 100

40 TCTAGTAGCC ATGTCTTGCA CTTCCCGAGT ATAAACGAAC TGAGATGCAA 150

24

ATTAAAAAAA GGGAGGATTT AAGAATAATG AAAAGAGAAA AATCAAGAAA 200

GCACAATCAC TAG 213

5 (2) INFORMATION FOR SEQ ID :6:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 345 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :6:

CGCAGGAGAA GGAACAGAGC CATTGTGCAT CCACTGTGGT CAACATTTAG 50

20 GAAGTTTTAA GCTAAGATTT GCCAAATTGT AGCCTACTGG ATTCCGGTTC 100

TCTTGACATC TCTTTCTAGT AGCCATGTCT TGCACTTCCC GAGTATAAAC 150

GAACTGAGAT GCAAATTAAA AAAAGGGAGG ATTTAGAATA ATGAAAAGAG 200

25 AAAAAATCAAG AAAGCACAAAT CACTAGTGTA GAGATAACAG AATTTCTGAA 250

TTCCCTGAAA CAATCTATAT AAATGCATGT GAAATAATAC ACCAGCATCT 300

30 GTGGCCCATTA CGTCACATAT TAGGAACTGA TAACATAAGG TAAAC 345

(2) INFORMATION FOR SEQ ID :7:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 159 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :7:

25

TCCATTTGAC ATCGCATTTC CATAGAAATG GCCAAAGAAA GAAGGTCCTG 50  
GGGTTTTTTA TAGAAAGCTC AAAAAGTTCA ACCTTTGATG CTATCCCCCA 100  
5 GCCCAATACA AAATATATAG AAAAAGCGAT TATTACAATA ACGCTTCAAT 150  
TTCTTTTCC 159

## (2) INFORMATION FOR SEQ ID :8:

10

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 15 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :8:

20

ATATTTCAAT CGAACAAAAA GGAAACTTTT TTTGAACTTA TTGAGGCTCT 50  
ACTTAAGTAC ATCGAAACCC TTAATGCTTC TGGGGCTGTG TTGATTTCTT 100  
25 TGCCTGGCTG GGGGTTTGAT TCGC 124

## (2) INFORMATION FOR SEQ ID :9:

## (i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 259 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

## (xi) SEQUENCE DESCRIPTION: SEQ ID :9:

CCGATACAAA TGTACGGAAT GTGTGAGTCC CTCTGGGAGC CCAACATGGA 50  
40 TCCGGATCAC CTGTTTGAAA CCATCTCCCA AGCCATGCTG AATGCTGTGG 100

26

ACCGGGATGC AGTGTCCAGGC ATGGGAGTCA TTGTCCACAT CATCGAGAAG 150  
GACAAAATCA CCACCAGGAC ACTGAAGGCC CGAATGGACT AACCTGTTC 200  
5 CCAGAGCCCA CTATATATTA TTTCTACTTC ATCTATATAT TGCAAAAATA 250  
GAAAATAGA 259

## (2) INFORMATION FOR SEQ ID :10:

10

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 216 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 15 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :10:

20

GTCACCAAGA CCGAGGCCAA ACTGGGCACC TTCCCCAGGG CCCTCAAGAA 50  
GCTCCTGCAC ACAATAAAG CGCCCTCGTT CTTTAGCAAG TCTGCTCCCT 100  
25 CGAGGCCACA GCAAGCCGGC TACGGAGCCC CCGTTCTGTT TTGAGCCGAA 150  
GACTACTTTA TTGGATGCGG TGAAAGGCCT CAGCTCTGAC ACTCTGATCA 200  
CTGTGACAAG GGGCCC 216

30

## (2) INFORMATION FOR SEQ ID :11:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 205 base pairs
- 35 (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40

## (xi) SEQUENCE DESCRIPTION: SEQ ID :11:

27

CACACTTCTT AAGATACATC AAGTACTAGT GATCTTTGCT AGCAGTTATG 50  
CCTGTTTCGT GTTACAGATT TGGCCATATA TTGACTAAAC AGCCCCTGTA 100  
5 AAGTTGAAAG AAAAAGTTTA TAACAGTGAA CTTCTGAGGT TTACGTTACT 150  
GCAGGCTTTG TTGAGAAGAG ATTGTTACAG TGTGATTTAT GGATGATCAG 200  
GGATG 205

10

(2) INFORMATION FOR SEQ ID :12:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 267 base pairs  
15 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID :12:

TGCATCTGAA GAGTTGATGA TCGAGACTAC AGCTGCACTA TCAGACTGTC 50  
25 AGGCAGCTCC CTCAGAAACA GCTTCAACAG ACTGGCTGCT GAGCAGACAT 100  
CACCGTCCTT CCGAGCTCCA CGGCGACTCC ACTCTCGAAC TTCAGTCGAA 150  
GTTGTTCCAC CACCTTCACG TTACCATTCA CCCTAAAAGA CCTTCTTGGG 200  
30 TAAGTCCATG CTGCGTCAAA TATTCCACTA TATTCCACAC TACTGCTGGA 250  
TATGCCATTC TCGGTGA 267

35

(2) INFORMATION FOR SEQ ID :13:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 116 base pairs  
(B) TYPE: nucleic acid  
40 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :13:

5 GCCTCATCAG GTTTGCCCAG ATGCTGGAGA AGGTGTGCGT GGAGACGGTG 50  
GAGAGTGGAG CCATGACCAA GGACCTGGCG GGCTGCATTC ACGGCCTCAG 100  
CAATGTGAAG CTGAAC 116

## 10 (2) INFORMATION FOR SEQ ID :14:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 296 base pairs  
(B) TYPE: nucleic acid  
15 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## 20 (xi) SEQUENCE DESCRIPTION: SEQ ID :14:

TTCGAACTTA CCAGCATCAT GTTTGGTCTC TTCGTATGGT CAAACTTCAA 50  
CTTTATAAAA ATAGTGAATA CCACTTATTG AGTGCTTAGA GTGTACCAGG 100  
25 CATGGTGCTA AATACTCTCT ATCCATTATC TCATTAAATC ACATGACACT 150  
ATGAGAAATG TACTATTCTT ATACCCACGT TGCCCAGGGT CATACATCTA 200  
30 AGGGGTGCAA GGACCAGGCT TTGATTTCAA ATTATAATCT AATGCTCACT 250  
CTCCAGGCCT GATGTCACGC AGCTCCTCAT TCTTATACTT AACATA 296

## (2) INFORMATION FOR SEQ ID :15:

35

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 123 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
40 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :15:

CGTCAGTGTG CTA CTT CACA TCATTAGCGA GGCCAGAAA CTTGAACAGG 50  
5 AAGTCCGGCA CTACCAACAT GCCGCCACTC ATACAACTCA ACTCTTCCTC 100  
CAAACTCGAT TCAAAGAGCA ATA 123

## (2) INFORMATION FOR SEQ ID :16:

10

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 262 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
15 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :16:

20

CAACACATTA GTGCATCAAT ATGAATTACT TGTTTAAAAA ATCAAATGCT 50  
GGCATTGTCA GAAAAATTTA ACAGGTTTAT TTATAATTAT CATAAAGTTG 100  
25 ACGCTGAAAC TTGTTCACTG AAACATTTTA ACTTGCATTA ATGCTTTACG 150  
TCTCCGCATT TATATTAAAA ATTCACACAC AAATGAAATG GAAAAACTGC 200  
CAATACCTGA TTTCTGTCCC TATTTTTCAC TCGCAATCAT ATACTTAGTA 250  
30 CTTTGTACTC TA 262

## (2) INFORMATION FOR SEQ ID :17:

35

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 169 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
40 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :17:

5 TAGCCAAATT CTAGGGCATC CAGATGCATT TGAGCCAGTC GTAATCCAGG 50  
AAATGTCAAA AAAGCCCCAA TGAATGAACA GAAATAGCC AGGAAAAATT 100  
TGAAAGTAAG TTTTGAAACA GGAATCGTGG AGATTCTAAA CCTTGCATTT 150  
TCAAGAAACG TGCATCAGC 169

## (2) INFORMATION FOR SEQ ID :18:

## (i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 221 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID :18:

AGGGGCACCA TTACCATCCA TCTGACATCG CATTTCCATA GAAATGGCCA 50  
25 AAGAAAGAAG GTCCTGGTAG GTTTTTCATA GAAAGACTCA AAAAGTTCAA 100  
CCTTTGATGC TATGCCCCAG CCCAATACAA AACTACACAG AACAAAGCAA 150  
TTATTAAAT ACTGGCTTCG GTTCTTTTTT TTCCTTTGCA AAGTTTCCTA 200  
30 CATATATGTC TTTTACAGTA T 221

## (2) INFORMATION FOR SEQ ID :19:

35

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 135 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

## (xi) SEQUENCE DESCRIPTION: SEQ ID :19:

1 TAGGCTCTGT GACGGCATAG TTTTCAGTAG CTTTATCACA ATATTCACAA 50  
5 TGGAGAATTA TATGACATGG TAGCAGAAAT AGGCCCTTTT ATGTGTTGCT 100  
TCTATTTTAC CTGAAATTGT AGATATAGGG TAATC 135

## (2) INFORMATION FOR SEQ ID :20:

10

## (i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 314 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :20:

20

GTTATCTATC TATCTTGCGAG TTTACCTATC TGATCTGATC TCTGTAATTA 50  
TAGTTCTGTC ATTTAAAATA TACTATTTAA ATCTAATTTT TACATTTCAA 100  
25 AAATTATCTT CAGTAGTAAC TAAGTATATT TTCTGTGGAT TCTGAGAATG 150  
TTATTTTTCA GAATGTGAGA GTACATATGT ACATTTATAA TCTTGTGACT 200  
TTAAAGTCTG TTTTCAGATA CAGTATGTAA ATACTTGTA AAAAAATTGT 250  
30 ATAATTTTGT GATAATGTAG TTTCCCAAAA CACATTTAGA AAGCATTATG 300  
TTATTAGTAA ATGA 314

## 35 (2) INFORMATION FOR SEQ ID :21:

## (i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 178 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :21:

5 TCTTCGCATC ACGCAGTACA GATACTCTTT CTGTACTTGC TTAATCTGCT 50  
TTTTGGCATC AGTCAGTTCT CTTTCAGGTC AGCATAATCT TCTTCCTTCC 100  
TCTGAAGATC TGCTTTCAGA TTCTGGGTAC GAGCAGAGCT TACAGAGAGT 150  
10 TCCTCTTTCA ATATTTCTGT TTCTTGCC 178

## (2) INFORMATION FOR SEQ ID :22:

## (i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 188 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID :22:

ACATCTGATA TCCACCTCCA TGACAGACTG ATCACACCTC CTTCTATACT 50  
25 ACTTCTGTTC TTTGTAAATA CTTAGTATTT TCCAAGGGAG TGTGAGAGAA 100  
GAAATGCTAG GTTCATGAAG GGTCTCTAGG TTAAACTTTC TTTCTTTTTT 150  
30 TTTCTTAAAA CAACACACTT ATTATCTTAC AAATCTGT 188

## (2) INFORMATION FOR SEQ ID :23:

## (i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 152 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

## (xi) SEQUENCE DESCRIPTION: SEQ ID :23:

TTCCANCTAA ACATCCAATA TNCNTTTAN TGCTTTTATA TTTTNAAT 50  
5 GTTAAACCC CTATACCACC TTTGGGAAT GTTTAAATT CTCCAATTT 100  
TCGTTATATA GGATCAACCA ACTAAGAAA GATTTTATCA ATTGAATTGA 150  
GG 152  
10

## (2) INFORMATION FOR SEQ ID :24:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 83 base pairs  
15 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID :24:

ACAATACAGA GGACAAAGAC CCCTCACAGA ATGCTTTTCA ACCAACTCA 50  
25 ACTTTTGCAC ACTTTTCAA CGGTCCCACC ACA 83

## (2) INFORMATION FOR SEQ ID :25:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 176 base pairs  
30 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

## (xi) SEQUENCE DESCRIPTION: SEQ ID :25:

AAATGTCCAT TGCTGTATTG CGTGACCGTG GTCCTTGCT GTCAAATNCA 50  
40 ACAATGACCA AATGATGATG CGCCCTTAAT ACCAGGATGA GACCAAACCT 100

34

ACACATCTCC CAAGTGCCGA ACAAAAACCT GAACAAAAAC CATNTGCACC 150  
CTACATCTGG CTGACATTTA CATTTT 176

5 (2) INFORMATION FOR SEQ ID :26:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 232 base pairs  
(B) TYPE: nucleic acid  
10 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :26:

AAATGTATGA TCAGAAAATA GGTACGCTTT TAAATATTT GAACAGAAAA 50  
GCTACAAATA AATNGAGCAA TGCTTTTAAA ATCATCTTTG TTTTATAGAC 100  
20 TTTTCTCGC ATGAATTACA TTTTACAATT TCATNNGGCA TATTCGCACT 150  
TTAAGTACTG ACGAAGAAGA CTAAAACAAT CATTTTTTAA CAATATTTAA 200  
25 AAGGATCATA TAGTCGACTT TTA AACANC CC 232

(2) INFORMATION FOR SEQ ID :27:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 192 base pairs  
30 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :27:

GAGAAAGTCC TTGCCATTCT AAAAGCCACC CCACTTCTCT AAGGAGAATG 50  
40 GCCCAATCTT CCCAAGTCCA CACAGGAGGG AAACATTGTT TGC GTAAATA 100

CGCAATGCAA AATTTNNTAT CTTGGCTTAA TACNNCGACG TTTTATTTTCG 150

AATGATGAGC CTTCTGCCCC CCCTTCCCCT TTNNNCTCCC CC 192

5 (2) INFORMATION FOR SEQ ID :28:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 201 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :28:

TAACACTTTA ANCATCTCTC CAAGCCAAGG AGGCTATGAC ANTGTAGCTT 50

20 TTATACTGTC CCCATCGGCC ACAATAACAA ACTTTTAACC CTCATAAAAT 100

GAATGAAATC ATCTTTCTAA GAATCTATAC CTACAATTCT CTGAACTAAT 150

CAATGAAAAA GATGATCAAT TCTGACTAAC AAAGATATAT CGATTCCATT 200

25 T 201

(2) INFORMATION FOR SEQ ID :29:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 275 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :29:

AACCTAAGGC AGTTGACCCC ACCTTCCAAC ATGTTTTTCAC TTTATTGGCC 50

40 CCTCCCTACA TTCGGGTTAG GTTCCATTG ATTTGCACAA TAATGACTTT 100

36

ATTCTCTTTT GATCAGGATT TGGCACATAA AATCCTTTTA TCATAGAACT 150  
AACTATTTTA ATTACATATA ATGTAATAA TGGAGAGATT TATAGAGAAT 200  
5 TTTGTTTTTT TGTCATATAC TCCATTTCGA AGACAGATAT GATAGAACTA 250  
GAAATTAAGT TGCATTTCTG CAAGT 275

## (2) INFORMATION FOR SEQ ID :30:

10

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 15 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :30:

20

GTAAATNTAC AAAGATAACG TCGCAATTTT CTTAGATTTA AATCAAAGAC 50  
ATTCATCAAC AAGATTTCGA ATGGAATATT CCAGAAATTT CTGAGCCATC 100  
25 TGATCACAAC AACCGTCTTT GA 122

## (2) INFORMATION FOR SEQ ID :31:

## (i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 197 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

## (xi) SEQUENCE DESCRIPTION: SEQ ID :31:

GGATTTGNAG CTTGAAGTTC AGAGCTGGTT TACCCAAAAA GGGAGCCAAT 50  
40 AGAGATCTTC CCAATGAACC TCAATACACG ATCGTAATAC TCGCACAATG 100

37

AAATGTTAAG TATGATTCTA GACTTCACTG ACTATCACAA TGATATTTTC 150

TCGATCGCAC TAGTGCACAA CAAAACACGA TGAGTGCAAT GTGAAAC 197

5 (2) INFORMATION FOR SEQ ID :32:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 97 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :32:

ACAAAAGTCT GAAGAAATCA CCAACNACAA GACGATTAGA AAATATGTTG 50

TTGGGGTCAC AACTAAAAAG TCCCTGATCT ACATTGNNTT TCNACTC 97

20

(2) INFORMATION FOR SEQ ID :33:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 260 base pairs

25 (B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :33:

CAAATAAAAC AANTNTTGTA AAGCTACAAT AGTTATATAC CAAAGCAATA 50

35 CCTATTACAT GCTTTACACA ATCCCATGAA AAAATAATTT AATAGCTCCT 100

AATCCCTGAT GCAAGGCACT TCAAAGCACC CGCACAAAAC TCCATGAAAC 150

AACATACAAT ACATCATTTA AATAACATAA ACGACTTTCA CACACTTGAC 200

40

CTAGGAAAAA ATAAAATCCA TACAACCACA GCTAAAAACA TGTTAAGATT 250

CACAATAAGA

260

## (2) INFORMATION FOR SEQ ID :34:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 168 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
10 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :34:

15 GGACNTGCGC NNNANNNANA GCCANTGAAC NCAGCCACCA NTGCAAGAAG 50  
ACTGCCTCTT NCCAGGCAAG ATTTTACTGG AGCAACANAA CCGGAGGTGT 100  
GATCCAAAAT ACCTTCCTTN CCAAGCCCGG GGTNNNNGAT AAGGTGTGGA 150  
20 NTTNGGTAA AGACAAGG 168

## (2) INFORMATION FOR SEQ ID :35:

- 25 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 173 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
30 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :35:

35 CTCGNACACT GTGGAGAGCC TCGNNNNNN NNGGTNTACT CAGGGGGACG 50  
AAAAGGAGNN GAANAAGTGA CACNGCNGNT AGCAGAGNGC ACAGAGCTGT 100  
GCTNNNGTGG TCCCTTAGNA SCCGAGNAGG TGGGCGCGAG GTGAANAAGG 150  
40 TGCNNGTGCG AGAGTGCGTG ATT 173

## (2) INFORMATION FOR SEQ ID :36:

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 134 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :36:

AGCAAGTNNN NNNNNNCATC CTGAAAGTCA AAATGGAATT TGTGTTTATA 50  
15 CAACTAATAA TGATTTTAT TTGCTCAGTA CAGACTNATT TACAATGAAA 100  
GTTTTGCTAA CCTTGGTAAG CTGTTTACC GTTT 134

## (2) INFORMATION FOR SEQ ID :37:

20

## (i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 160 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :37:

30

TGGCGCCTGT CCGAGAGCAA GTNGNNNNNN NNCCTGAAAG TCAAAATGGA 50  
ATTTGTGTTT ATACAACTAA TAATGACCTT TTATTTGCTC AGTACAGACN 100  
35 GATTTACAAT GAAAGTTTTG CTAACCTTGG TAAGCTTGTT AACCGTTTAC 150  
ATGACTTCTT 160

## (2) INFORMATION FOR SEQ ID :38:

40

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 base pairs

40

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :38:

CTAGTTTAAT GAATCTGAGG GGCTACTATA AACAAATCCCA CCCTCACACG	50
ATTTTTTACC TTCNTTACTT NGCCCTTCAT TAGGCAACCC TAGCAGCACT	100
CCACCTCTAT TCTCGCACTG TCCAAGAGGC CCACCTAATC	140

15 (2) INFORMATION FOR SEQ ID :39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 203 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :39:

AGCAAGTATC ANNNNNNNNN ATACATTTGA ATTCAAGTTG TTTTTTGTCA	50
AATTGTACAG TGTGTCAATT GATCTTCAAG CTGNNGGTGC CTAGAAATGG	100
GNCGGTGTCT GTAGCCCTGG CATGTGCACA CGGAGCATTT GCCACCACCG	150
CAAGCAAAAA GTCTGGGNGA AGTTCACCAA NGNCAAGAA NATTANGGGA	200
AAA	203

(2) INFORMATION FOR SEQ ID :40:

(i) SEQUENCE CHARACTERISTICS

- (A) LENGTH: 170 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

41

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :40:

GAAAAGCNNN NNNNNNNGGC TTAAAGAACA ATATGCTGAG ATGGAGAAGG 50  
ACCTAGCGAA ANTNNNAACC TTTTAAGAAC TTGAANNACA ACAATCACAA 100  
10 ACTAATGAGA AGATGTTTAC CTCTCTCCTG AAAACTATGC CCACCAGACC 150  
GTTTAGCCTC TGCTCAAGCT 170

15 (2) INFORMATION FOR SEQ ID :41:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 270 base pairs  
(B) TYPE: nucleic acid  
20 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :41:

GCTGCATGTT TCCTTGNATT TGAGCTTGAA AGTTCAGAGC TGTTTACCCA 50  
AAAAGGGAGC CAATAGAGAT CTTCCCAATG AACCTCAAAC ACGTCGTAAT 100  
30 ACTCGCACAA TGAAATGTCA AGTATGATTC TAGACTTCAC TGACTCATCA 150  
CAATGATATT TTCTCGATCG CACTAGGCAC AACAAAATAC GATGAGTGCA 200  
35 ATGTGAAACA TCTACAAAGT AAATCACACA CTGTTTTTTT AAATNCATAG 250  
AAATTTGATT TGTAATAAAA 270

(2) INFORMATION FOR SEQ ID :42:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 245 bas pairs

42

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :42:

AGAGCTGCAT GTTTCCTTGA TTTGNAGCTT GAAGTTCAGA GCTGTTTACC 50  
10 CAAAAAGGGA GCCAATAGAG ATCTTCCCAA CGAACCTCAA TAACGATCGT 100  
AATACTCGAC AATGAAATGT TAAGTATGAT TCTAGACTTC ACTGACTATC 150  
15 ACAATGATAT TTTCTCGGAA TCGCACTAGT GCACAACAAA ATAGATGAGT 200  
GCAATGTGAA ACAATCTCAA AGTAAATCAT ATACTTGTTT TCTTA 245

(2) INFORMATION FOR SEQ ID :43:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 124 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
25 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :43:

30

TACTGNGA AAATGTACAA AGAAAGTATC CCCAAATNAT TTACAAAGCC 50  
TAAATGTCCT TGATACACAT ACACGGNAGT ATGCAGACAA CAAAGATTAA 100  
35 ATGAAGACAC TTTACTTTT TCGG 124

(2) INFORMATION FOR SEQ ID :44:

(i) SEQUENCE CHARACTERISTICS:

40

(A) LENGTH: 144 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :44:

GAGTTCTCAC GAATACACAG GTTCAGAGAG ATGAGANGGA ANAACATAAG 50

GCAAATTCCT AACANNCGCT AATATAGGAG GCCGCTCGAT AGGATTTTAA 100

10

AAAAATAAAA ACAATCTTAA TAGTGGGACA AGGCCATCAG AAAA 144

(2) INFORMATION FOR SEQ ID :45:

15 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 177 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :45:

25 ACTGATTCNN NNTGAAAATA CCCCCTTTCT CCATTAGTGG CATGCTCATT 50

CAGCTCTTAT CTTTATATTC CAGTAAGTTA TTTTGCTCTC ACTGTTTTAA 100

CAAAAAAAAAA AACAACAACA TAAAAATCCT TGCAAACCAT GTCAATTGGA 150

30

GAAATTTAAT GTTTTTCATA ACATGAA 177

(2) INFORMATION FOR SEQ ID :46:

35 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 256 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

40

## (xi) SEQUENCE DESCRIPTION: SEQ ID :46:

ACTGATTCTG CGAAAATACC CCCTTTTAT TAGTGGCATG CTCATTCACT 50  
5 TTATCTTTAT ATTCAAATAA GTTATTTTCGC TTTCACGTGTT TTAACAAAAA 100  
AAAAAAAAAA AAAAAAATAC AGCCCTCCCC AATCGAAGAT TTCAACTTTT 150  
TAATTCACAC GGAAAAACCA AGACAATTTT ACAACTTCTG GACACAACCA 200  
10 TCAACACAGG ACATTTTTTTT TACAGGCAAA TCACTTAAAA CAAAAAAGAT 250  
CCCAGA 256

## 15 (2) INFORMATION FOR SEQ ID :47:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 155 base pairs  
(B) TYPE: nucleic acid  
20 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## 25 (xi) SEQUENCE DESCRIPTION: SEQ ID :47:

GAGAAAAGTC NNNNNNNNNA GGTTAATCTA ACTTTTCTTG CTTATTTTCAG 50  
CTATGATCTG AAAGGATGGA AGACACAAAA TGTATGNNTA AGGTATTTTT 100  
30 AACAAAGATA CATGGGTAAA TTAACAGCAG TAATGTAAAA AAGACTGAGG 150  
AGCAA 155

## 35 (2) INFORMATION FOR SEQ ID :48:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 68 base pairs  
(B) TYPE: nucleic acid  
40 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :48:

5 GCTTATTTTA CTATATCTAA AGGATAAAGC ACAAATGAT GAATAAGATA 50  
TTTNNACAAA GATACACG 68

## (2) INFORMATION FOR SEQ ID :49:

10 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 244 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear  
15

## (xi) SEQUENCE DESCRIPTION: SEQ ID :49:

20 CCTGAAAGCA AAGCCATNNA AAGCTTAGAG ACAAGCACNT GAGATGCAGG 50  
GGCCTAGCTA AATTNGAAC CTGNTGGAAC TTGAACCACA ACGATAAAAA 100  
ATTACAGAAG AGTTCACCTC TTTCTGAAAA CTATCCACAG ACCGTTTACC 150  
25 TCTGCTTCAA GCTANCAATA TATCAATGGC ACTCTCATAN CAGAAGAAAG 200  
AAGTTCCTAC TAGCTCCTGA TTATATTNAA GAAGATGCCC ATGG 244

## 30 (2) INFORMATION FOR SEQ ID :50:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 81 base pairs  
(B) TYPE: nucleic acid  
35 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## 40 (xi) SEQUENCE DESCRIPTION: SEQ ID :50:

ACTCGNNCAG CGATAGTCGG AGCTACCAA CAAAAACNCT NNNNCAGAAA 50

46

GGANAAAGNG CCGCCCTACG TGGTACACAC A

81

(2) INFORMATION FOR SEQ ID :51:

5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 223 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :51:

15

GTACTTACTG CACTATGAAA AGCAATAGAT CGTCCATAAG TTATAACCAA

50

AATCTCTCCC TCAGGAATAT ATTCCATACT ACTAACAGAC ATATTAAAT

100

TTAGAGATTT CACTTCTGTC ATAGTAGCAT GATCCCAAAG TCGAACAGTT

150

20

TTGTCATCAG CAGAAAGAAT CTGTTTATCT CACTGCACCA CAGAGCTTTT

200

TTATACCAGA AGNATGACCA CTG

223

25

(2) INFORMATION FOR SEQ ID :52:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 49 base pairs

(B) TYPE: nucleic acid

30

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :52:

TATGGTTTNT TGTAAGAAAAG CTCANNNNANA AAGGGANNIGG CTTAAGAGA

49

(2) INFORMATION FOR SEQ ID :53:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 213 base pairs

47

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :53:

10	CAACGTCAGA GCACACNNNN NNCTCAGNGC ANAGGCATGA CAGGAGCTCA	50
	TANCNATAAG CCATATAANN NTGTTACCTG TATAGAATGA TGAATTATCT	100
	TTCTAGAGTC TATACCTACA GTTCTCTGAG CTAATCAATG GAAAAGATGA	150
15	TCAATCTGAC TAACAAGAGN AATTGATTCA TTTTCTTCCA CNCCCCTTCA	200
	TTCAATAATC AAA	213

(2) INFORMATION FOR SEQ ID :54:

20

(i) SEQUENCE CHARACTERISTICS:

	(A) LENGTH: 166 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
25	(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :54:

30

	GCGTGTGTG NGGAGTGGNN GTCTNGTCNT CCTGTTAAGG TTTTGTGTG	50
	CGTNNTTGC TANGGGGNGG GTTNGGCAG GTGTTGCCGG TAGCNAAACN	100
35	GTTGGCCCCA TNGCCNGNAT TGNNNCCCN CNNGGGAANG GGGGGGGNGA	150
	CCNAGNGGG AAAAAA	166

(2) INFORMATION FOR SEQ ID :55:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 75 base pairs

48

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :55:

ACCTCATAGC GAACTCGTCN TATAGANNNN ANNTGAGTCG AGCTCGATGT 50  
10 NGNCGTTGTN GCTGCCAAGC GACAT 75

(2) INFORMATION FOR SEQ ID :56:

- 15 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 181 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :56:

25 AATNNNNNCC TATTTTGTA TTTTTTTGAA AAAAGTTCAA TGTTTCAGTTT 50  
TCCTTAGTTT TTACCTTGTT TTCTCTATAG GTCATGATTT CTGTGAAGCA 100  
AAAAGATGCC TTTTACCATG AATTCTTGAG TTTACATCAA TAATATTGTA 150  
30 TATTAAGGGG ATCAGAAGTA GGAAGGAAAA A 181

(2) INFORMATION FOR SEQ ID :57:

- 35 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 130 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

## (xi) SEQUENCE DESCRIPTION: SEQ ID :57:

TCGAAGAGAC CTCAATCACC GTTTTTCAGG ATGTTTGATC ACAATACGAA 50  
5 GATGACGNNNA TCCAATTTCA GAACACCACA GGGCACTGGC ACACAGAGGG 100  
GATTATTACA GAACCACTGA GATGACATTT 130

## (2) INFORMATION FOR SEQ ID :58:

10

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 15 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :58:

20

GTNATTTTGA AGGTCTCACA AATNTAAAGA CTTATTGTAG CCCATGAACA 50  
CATTGACAAG TACAAAAATT AAAAAATAT GCAGAAATAT TGAATAACTA 100  
25 GAACACAAGC CACTGTTTCA ACTCCAGAAA AAAGAAAGGC TTTACTTTTT 150  
CCATGAA 157

## (2) INFORMATION FOR SEQ ID :59:

30

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 252 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 35 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :59:

40

GAGGTGAAGT TGTTCCTTTAT TGAATTGCAT TATNAATGNA TAGGCTGTGC 50

50

CTTTTTGNAC TCTCTATGAG TTCATGAATT TAACCAATAC GNCCACAAAT 100  
GCTGCTGCTG TCACAGAGAG ATGCCGATAA AGGACACCCA CCACCAATTT 150  
5 TTGAACAGGG AGGGGAGAAT CAACTCTGAA TGTGATGCAG TGACCAGGAG 200  
AGAGGACCAT GTTAACAACA CCACACAAAT GCAAATGACT NGTTCTNAAA 250  
CA 252

10

(2) INFORMATION FOR SEQ ID :60:

## (i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 198 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :60:

GACCTCGTTT TTCATCCTAT TATGGCGTTT ANCAGGCTAG ACAGAAACAC 50  
25 GCCTTAACTT TANTTGCCAC AAATCTTAAT ATTTTCTCCA CTAATATTAG 100  
AAAGGAAGCA ACAAATAATG TCGCTTTTCA CCTGACGTCT GGTTCAACTT 150  
TCCGCCCAGC CTATTCCTGN GTCTTCCTCC TGCCTTTCTA ATGTCCCA 198

30

(2) INFORMATION FOR SEQ ID :61:

## (i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 229 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :61:

51

GAGGTGGCAT TATGTGAGAC AGCATTGTTT TAGGGAGTGC CAAGCATTCT 50  
 ACAGCATTG ATGGTGGAAA TAGTCATGCT TTTTATTTCT GCTCTCTAGG 100  
 5 AATGTAAGGT GCACAGCAGG TCAGGGTACT GCTGTGTGAG ACAAAGGTC 150  
 CAGGTAGAGG CAATTCCCCA GATGCAGGCA GGGCAGGTGC TCACTGGGCA 200  
 GAGTGCTTCT CATAACCTT CAGGAACCC 229

10

(2) INFORMATION FOR SEQ ID :62:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 181 base pairs  
 15 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :62:

CATCCTGGGC CCTGGCCGAT GTGCATATCA ACANAAAAAA GGGACTGAAG 50  
 25 AACATCGGCC ATATCATCCA CACAAGCCAA ATCTCACACC TTTACTTTAA 100  
 ACCGCTTAAT GAATTCATG ACCTTGAGGG CTAAAGATCG TTCTTCGGGC 150  
 AAGAGCTTTT GGACTGTTTT TAGAACAGAA T 181

30

(2) INFORMATION FOR SEQ ID :63:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 180 base pairs  
 35 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :63:

52

GTTGATTGTG AATCATCCCT CTAACATATA ATCAANANTA TGAGTAGAGA 50  
 ATTTGGCAGA AACAAAGAAA GGACATGGGA TAACTTTTAG ATTTAAAGAG 100  
 5 GCAGGCTTGG AACACAAACT GGTATTCTGC TGACACACTG CTGCATATCA 150  
 TAAGGCTACT CCACAAGACC ATTAGAAGTC 180

## (2) INFORMATION FOR SEQ ID :64:

10

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 15 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :64:

20

ACAATGTTCC AACATATATA TGGGGAGGGG AGAACANTTA TCTGTATAAC 50  
 AGGGAAGTGT GATTATTTAA AAATANGCNA GAACTTATTT CANCTGTGCT 100  
 25 TTAGAAANAA NTGTATACGG 120

## (2) INFORMATION FOR SEQ ID :65:

## (i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 70 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

35

## (xi) SEQUENCE DESCRIPTION: SEQ ID :65:

CACATCGCTA TAATCCTTTC TGAGGACTTA AAACCTTATN CCACTTACCT 50  
 40 TTATGACTTT TAACAAGCCT 70

## (2) INFORMATION FOR SEQ ID :66:

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 240 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :66:

TTTCGAGCAA AATGTTTACA TTTACATGGA AATACACACT AAAACAGAAT 50  
15 ATTTTCCTAA TCATGAAACT TCGCCAAAGC AAAATACAAA CTTCCAACGG 100  
GAGGTCCACT CAACTAACAA CAATGATCCC CAAGCAGGGC ACCAAGAAAC 150  
CTGGGGGACC CTTTNCAAAA AACCTCCTTT CAAGAGACCC TAATACTCTN 200  
20 TCCACACACC CACACGATTT AGGAACTTGG ACATGTCCT 240

## (2) INFORMATION FOR SEQ ID :67:

25

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 254 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :67:

35 GGAAGCACTA CATTTTCATCC AAAGCTGGGT TGAGTTATTT TTGAACACTT 50  
TACGATATGC TTAGGTAGGC TTTTAACTTG CTCCTCCAAA CAATATCTNT 100  
TGGGAAAACA AGCCCTGTGG AGAGATCCTT CCATCAAGTC GCTTCAATTT 150  
40 AACCTATTTT TAGAGGACTA GACATGCAGA ATCGTCAACT ACAGGGAATG 200

54

AAAAGTTCAA AAAGTAGATC CTACAAGATG AACGAGTACT TTTCTAAACA 250

TAAG 254

5 (2) INFORMATION FOR SEQ ID :68:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 192 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :68:

AGGCACCAAA GAAACACCAA GCAATAAAGT GAAAGACTAA CCAAGATTTG 50

ACATTGTATG NTTACTGTAT TCTTTAAGAA ACAACTACAA AAAGAAAATG 100

20 TCAACAAATN NNNACAACCTG AGAACCTGGG AATTCCCGCA CGGAAGACAA 150

GAGATAACCT CTCCAATTTA ACACCGCTAG GNTTCTATNN TA 192

25 (2) INFORMATION FOR SEQ ID :69:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 112 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :69:

AGCAGCGNNN NNNNTNNAAC CAAAAGACAG GAGCAGAGAG GCCTGAGAGC 50

AGGAGGCGAA TTCGATCTCT CCTCACAAAC AGCCCAGGAA AATATACACC 100

40 CCGGGGGAAG CC 112

## (2) INFORMATION FOR SEQ ID :70:

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 232 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :70:

AAGGGTCTCC AATTTAATCC TTGGGTGTT TTACCACTTC TTTCGTAAAT 50  
15 TTATCAAGAT TTCTTTCGCA CAAATACTCT AGCGCCTCAC AACAAACCTG 100  
ACCTTGCGCA GGAAGTCGAC CATCAGCACC CCCTTTACAA CATCGTTCAT 150  
ATCACAATTG AGAAGATGAT GAATGAAGAT TCGCTTCCAA GTTCCAAGGG 200  
20 CAGATTTATT CCTTTAACTG ACATTTCCAT GA 232

## (2) INFORMATION FOR SEQ ID :71:

25

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 160 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :71:

35 CNTGGATCCG NCCTTGTTAC GNCCAGGACG NCTGGACCGC AAAATGAATT 50  
TTCACCTTTTC GACCACCGCC AGAAGAGATG ATTTTCTCAT CATNAACAAG 100  
GAACCTTTGA GGAGATCGAC TGAAAGACTA GCGNCCCNGT CAGATAAGAT 150  
40 TTAGGGCTGA 160

## (2) INFORMATION FOR SEQ ID :72:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 182 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :72:

AAGGAAGACT GGTTCGCCAT CCGAGATCAT TAAAAANGNC TGACCCTAAC 50  
AATACGTACA AAAATATAAA ACGCAAATAA AAAATACAAA CAGATTCCTT 100  
CTTAAAGTAC TTTTAAGAAA AAAAGCAGGN CCTTGGAAGT TTCGATTCTT 150  
TTTTCTCTCC GTCGCAAATT CTATGTTTGG AT 182

## (2) INFORMATION FOR SEQ ID :73:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 168 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :73:

CAAGAGGCAG CTGCCCCCTCC CACCTCGGAG GNCTGAGAGG GNCTGTGNCG 50  
ATGAGCTGGA CGAGCACAGC ACTAAAAAGG CTGCCCCTNG CACAATAACA 100  
CTGAGAGGAT GATGAGAACA CNCTTGAAAT GCTTCATNCA CATGGGCAGG 150  
ANAGGCTGCA CAATGAAA 168

## (2) INFORMATION FOR SEQ ID :74:

57

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 221 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :74:

10

AACCTTTATT CATCCTCCTN TCCAAGACCT ATGAGAAGGT TCCAGGCCCC 50  
AGGAACACAG GCTTCTTGGC CCCAGATGCA CCTCCCTGCA CCCCAGGGGTT 100  
GTATACCACA CCCCAGGGCCC CTAATCCCAG GCCCCGAGAT AGGAAAGCCA 150  
ACTAGTTCTT TNTNTGTGAT TCAGTAGGCC TGACCTATAG NTGGAATGTC 200  
NCTNTCCCTN NAATAAATTN C 221

20

## (2) INFORMATION FOR SEQ ID :75:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :75:

AGACTGNTTG GGTCAATCCGA GATCATTAATA AATGNCTGAC CCTAACAATA 50  
GGCACAAAAA TAAAAACGAA ATAAAAAACC TCCTTANNTT CGAAGTATCT 100  
TAGAAAAAAA CAGGGCCTTG AGTTCTG 127

35

## (2) INFORMATION FOR SEQ ID :76:

40

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 180 base pairs

58

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :76:

AAAAGAACAG CAGTTTCACA TTTCACATAT TTGAAAAACA TTTCAAACC 50  
10 CTCTAATAAG TATTTAATGA AAATAAATTT ATCGAAGAGA AACAAATGACC 100  
ACAAAATTAA TACTACCAA TCATTACTGA GACTCTTGCA TTACAATATT 150  
15 TGGAGAGTAG GTGAAGAAAA TTAGACCGA 180

## (2) INFORMATION FOR SEQ ID :77:

## (i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 142 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID :77:

GATTAANNNN NNNGCACCCN NNATTACTGG CACAGCTGGT GAATATTTTC 50  
30 GTGGACTTTT GACTAGTGCA CCTGCGTGCG GGAAAACANT GATAAACTG 100  
TCACTTTAGC CNCNAACTAC AAGACCGTT AGACTAGAGA GC 142

## 35 (2) INFORMATION FOR SEQ ID :78:

## (i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 124 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :78:

5 GGGCCCTGAGA GCAGGACGGC GAATTCGATC TCCTCCTTCA CAAACAGCCC 50  
ANGGAAANTA CACCCCGGGG AANNCCCCNC NCNNTTAGAA CCNNCAGGNT 100  
CTGNCCCCCC CNNNGNCCCC CCG 124

## 10 (2) INFORMATION FOR SEQ ID :79:

## (i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 171 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## 20 (xi) SEQUENCE DESCRIPTION: SEQ ID :79:

AGGTATAGTG TTCCCTAATC ATGTACTTGT GAAGCACCCG GANTTTTTCA 50  
TATAGTCTAA AAGCTAGAAG AACAAGAGTG TATTTCGTGG GTGGATGTAT 100  
25 NGTCACTTGC TGAANNNTT GAAATACCAT TATCCCCCTT GCTAACNCCT 150  
TTAAGNAAAN GCCNTTTTAA G 171

## 30 (2) INFORMATION FOR SEQ ID :80:

## (i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 98 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## 40 (xi) SEQUENCE DESCRIPTION: SEQ ID :80:

CTGAACAGTG TGGTCGAGCA TTCCAAGTCC GTGAAGGTGC AGGAGCGGTA 50

60

CGACAGTGCC GTGNGGGCAC CATGGCACCT NGACCACGGG CNCCTAAG

98

(2) INFORMATION FOR SEQ ID :81:

5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 108 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :81:

15

CCTCAACAAG TGCGAGACCT GGGCGTCCAA CCTGCCTACA ACCACAGCCG

50

CGAAAGAAGA AGACCTGCTG CTTCAATACA ACACGGGAGG ACCTGGCCAT

100

CAACATCA

108

20

(2) INFORMATION FOR SEQ ID :82:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 180 base pairs

25

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :82:

ACACATNACC CACNGCCAGT ATATCTCGAA CAAAGTCTCA GACGATACTC

50

35

CCTCAATTG TAAAGCTTAA TACAGTTNT GGAAATCATT TAACACCCGA

100

GAATGTCCCA TCACAGTCTT CCGTCAAAT TTAGCCTCAC AACAACAACA

150

ACGCCTACGA AATTCTAAAT TCAGAAGGAA

180

40

(2) INFORMATION FOR SEQ ID :83:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 199 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :83:

10

GGCTTCTGAT CGCCATCCTT GAACAGGGCA AAGGTGGCCT CACCAGCCTT 50  
CGATGCAGCT GCCATGCGCG CCAGAATCAG CGAAGGCATA CCCTTACGTC 100  
GTTGGACGCA TGTTTAGATG CCTTTGAGAC CGCCCAGAGA AGTCCTTGTC 150  
CTTCTTAATA AACACCTCCT CGCCAACTGC GACGACCACA ATCACCGTA 199

## (2) INFORMATION FOR SEQ ID :84:

20

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 214 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID :84:

30

CTTCGGTAGT GCCGCCGTGG TGCCACACAC CGTTGAGGTT GGAGTGGGCA 50  
CAGGCATGGT ACCACCAGCC TCCCCGCTGG TACAGGGCAC AGTTACCTGA 100  
GGGGAGAGAG AGAGTCCATG TCCTCTCACC AGAATAAAAG CCTCTACCTG 150  
CACCTCACAG TGCAAGGCTT TTGCCAGGCA TCCCCTGGCC CCTCCCATTT 200  
NACNGAATAC AACC 214

40

## (2) INFORMATION FOR SEQ ID :85:

62

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :85:

10

CCTGGGCAAG CTGAATGTGA AGTTGACCAG GCTAACTGAG AAGCAAGCCC 50  
AGTACCTGGG CATGTCCTGT GATGGCCCCT 80

15

## (2) INFORMATION FOR SEQ ID :86:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 210 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID :86:

30

GGGGATAGCT GGCTCATCCT CGGAAAACAG ACCCACATCT CTATTCTTGC 50  
CCTGAAATAC GCGCTTTTCA CTTGCGTGCT CAGAGCTGCC GTCTGAAGGT 100  
CCACACGGCA TTGACGGGAC ACAGAAATGT GACTGTTACC GGATAACACT 150  
GATTAGTCAG TTTTCATTTA TAAAAAAGCA TGACAGTTTA TTACTCTGTT 200  
TCTTTTAATG 210

35

## (2) INFORMATION FOR SEQ ID :87:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double

40

63

(D) TOPOLOGY: lin ar

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :87:

CACAAAAAGC ATGATCAGGG CTAGCCTCAA TACAGGGAGA AATCATGGAT 50

ATTTAAAAAT ACTTTTTTTTG ATTCAGATTC CGGTATGACT GAAGANGCAA 100

10

CA 102

(2) INFORMATION FOR SEQ ID :88:

15 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 275 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :88:

25 GATAGGCGCA TGCATACTAC GGCTAAGGAG AAACAATGTT CCTACATATT 50

ACGGGCAGTG AGAACATTAT CTGTATAACA GGAAGTGTGA TTATTTAAAA 100

ATAGCAGAAC TTATCNGTCT GTGCTTTAGA AATAACTGTA TACAGTGTTA 150

30

TAAGTTGAAA AGAACTCAAA ATAATAATA CAAATAAGAA CCTACGTATT 200

AGAATTCAAA AAAGCTGCTT TCTGTGAAGT CAATCAGCTA TATTAAAAAA 250

35 TGACACAAAT TCAAAACACG ATCAT 275

(2) INFORMATION FOR SEQ ID :89:

(i) SEQUENCE CHARACTERISTICS:

40

(A) LENGTH: 263 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

64

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :89:

GCCTGATGGT ATATACTGTT TTGCAATTGC ATACAACTGT GCATTACAAA 50  
TTAATAGTAA TTATGGTTTG GNNGTAAAT CGAGTTTCAG AATAAAATNA 100  
10 AAAACAATAA AATCCAAAGA ACGATGTAAA CAAAAAAGCT TTTGTTTTGT 150  
TACAAAGTAT ATTAAGGATT TTCTGCTAAG ATTCAGTTTA AGAGTTTTCC 200  
15 TCGTGAAAAC TAAGTAGAAA CACAATGCCA ACAGCTGGCC AGTAATCAGT 250  
GCTGTGTACT CCA 263

20 (2) INFORMATION FOR SEQ ID :90:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 108 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
25 (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID :90:

GCGTCCTGCC CAACATCCAG GCCGTACTGC TGCCCAAGAA GACGGAGAGC 50  
CACCACAAGG CCAAGGGCAA GTGAGGCCGC CCGCCGCCCC CGAGGGACCC 100  
35 CTTTGAGA 108

(2) INFORMATION FOR SEQ ID :91:

(i) SEQUENCE CHARACTERISTICS:  
40 (A) LENGTH: 206 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double

65

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :91:

	GCCTTGGTGG AGGGCATGAG GCTATGATGA CTATTGGCTA TAATATGGAT	50
	ATGGCTTTGG CTGATAGATT TGAAGAGACC TCAATTACGT TTTTCAGGAA	100
10	TGTTTGATCA TAGATACAGA GATGGTGGTC CAGTTTTCAG AGCACCACAG	150
	GGCACTGTGT ACACATGAGG GGTTACCTTA CAGAGCCACT GAGAATATAT	200
15	TAATAA	206

(2) INFORMATION FOR SEQ ID :92:

	(i) SEQUENCE CHARACTERISTICS:
20	(A) LENGTH: 210 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :92:

	CCTTGGTGGG GGGCATGAGG CTATGATGAC TATTGGCTAT AATATGGATA	50
30	TGGCTTTGGC TGATAGATT GAAGAGACCT CAATTACGTT TTTTCAGGAAT	100
	GTTTGATCAT AGATACAGAG ATGGTGGTCC AGTTTTCAGA GCACCACAGG	150
35	GCACTGTGTA CACATGAGGG GTTACCTTAC AGAGCCACTG AGAATATATT	200
	AATAAANNNG	210

(2) INFORMATION FOR SEQ ID :93:

40

	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 189 base pairs

66

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :93:

AGGACTTCAT CCCAGACTCA CTTGTTCTGT TACAGAACT AACCTAAAAG	50
GCTGGAAATT AAAGGATACA ACCTAAGAGG TTATAACAGC AGACTGGTAA	100
AACATGGCGA AAGGAGCTCT CTCTTTCCCC GCAGTCTACC AAGCTCCTGT	150
GCATTTTCAC CACATAGATC TGCTAGCTTA CAAATGATG	189

## (2) INFORMATION FOR SEQ ID :94:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 160 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID :94:

GAAGTGACAG GNAAGCTACA GGTGTATAAC AAATTTGTAA ACTAACCAAG	50
CACAATGTGG CAGGGCCTAG CTGCTACAAA GAAGACAATT TAACAAATAC	100
TCAACGCATG ACAAAAAACT CAGGACTGCA TTTGCACTAA TCGATAACGN	150
GTCATTTAAT	160

## (2) INFORMATION FOR SEQ ID :95:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 171 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

67

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :95:

TGCTTTATAC ATNATNAAAG GTAGGCACTT CATAAAATTT GCATTTTGGT 50  
AAAAGGCAAC AATTTGATGT CAGTATCTTA ATTGTGTCAT TAACTTTTTT 100  
10 AAGAGAACAG ATTATCAAAA TTTTACGAAG AAGAAAAAAA NTATAGTTTT 150  
TAAGGAAACT ACAGAAGGGA T 171

15 (2) INFORMATION FOR SEQ ID :96:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 131 base pairs  
(B) TYPE: nucleic acid  
20 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :96:

GTGGATAAGA AGATGTGTAC TTGGGAACAA GGCTAAAGCC ATTGGCTGAT 50  
TTCCCCAACC TTTTATTTCG CGAAGAACT CCAGTTGTTA ACTTTTTGAG 100  
30 AGTTTTTTTTT GGCAAAAGAA CTNCATTAN C 131

(2) INFORMATION FOR SEQ ID :97:

35 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 279 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
40 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :97:

5 GTCCTAATAT TTCTGTNCAG AAATTGTCAA CTTGACTTGA GAGTTGAGAA 50  
 GTAAAGTTAA GGCAGTGACA ATATATCAGA ATGGAAGTCC TTAAGAGCAA 100  
 CTAACAGGTT CTTGATCAGA CTGACTATCT TTTCTTAAGT TCATAATATN 150  
 TTAAGTGTCCA GCCAACTATA CTTGGATCAA AATATCCTTC ATGAAGGGCC 200  
 10 ATAATGTATT GATGATCTGC TGTAACCTTG AGAAGCTTCC TGAAGCTCNT 250  
 TTTGAATAAA TTTATNGAAC TTATGAAGA 279

## 15 (2) INFORMATION FOR SEQ ID :98:

## (i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 266 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## 25 (xi) SEQUENCE DESCRIPTION: SEQ ID :98:

GTGAGTCTTT CTTCAACTAG GGGAAATGTTT CCAGGGCACG CCAGGCCTCA 50  
 CTCACGCAGG CCTCCGCGAC AACTGTTCAG CACTGACTGA GGATGAAGTG 100  
 30 AAATCCTGAA AGCTGAGAGC CAGCGCCCTC ACACGAGGGC TGGGACGTAA 150  
 CAAAAGCCCA TCAAGAGTTT TGCCCAGGGC TTTCTTGAGC CTTGAAGCAT 200  
 35 GACGAGACCA GGACCCTTTA GGATTAAGCA AGTTTTATGC GGTCTNAAAA 250  
 AACTCCAGGG CCTCCA 266

## 40 (2) INFORMATION FOR SEQ ID :99:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 206 base pairs

69

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :99:

GGGAACATTT ATTGACATGA AAAGGTGTTT CAGATATACT GATATGTCAA 50  
10 ACAAATAGTA AAACAACATA GAGTAATGAT TCATTTTGGT AAAAAATATA 100  
TATGTATATA TAGAAAAAAA TTCTGCAGGA CATATGCTAA ATTGGTAACA 150  
15 GTGCTTACCC CTGGGAAGGG GGTATACGAT GTTGATTAC TCTTTGGGTA 200  
CGTATT 206

(2) INFORMATION FOR SEQ ID :100:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 73 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
25 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :100:

30

CGCAACTNTC NCTAAACATC CAGTTTTCTA ATNTAATAAA AAATGGCAGT 50  
AATTATCCTC ACCTCTCAGG GAA 73

35 (2) INFORMATION FOR SEQ ID :101:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 108 base pairs  
(B) TYPE: nucleic acid  
40 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :101:

5 GAGCACAATC ATGNGCAAGC GCAACAGCAC ACCTTTATCC GAGTGAGACC 50  
ACTATGCAGC NGAACAGAGA CTTCTTATCT CTTCTTCTTG ATACTTGAAT 100  
ACTGCCCC 108

10 (2) INFORMATION FOR SEQ ID :102:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 210 base pairs  
(B) TYPE: nucleic acid  
15 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID :102:

GAATTATCAA ACCATCNTTG CTGACATTAA TTTTCCAGCT TTGATCTTAN 50  
NTCTNGCTTT AGTCCTCATA CAATGACTGT GTTTTCTCA AACGATNTAT 100  
25 CGTATAGGNA TCCTTCTAAG CAATCCTGCA CCCACAAAAA AGCTGCATCT 150  
TCAATATAAC ANAAAAAGGN ATTTTGCAA AAGTACAAGT TTTATGTCTN 200  
30 CTGTTAACTG 210

(2) INFORMATION FOR SEQ ID :103:

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 76 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :103:

71

CGTAGTTCGA TTCGAGTGGT CTATACAATC ACACCAAGCT TGATGTTGAT 50  
GTCACCAAAA TTTCTTTCCA AAAAAA 76

5 (2) INFORMATION FOR SEQ ID :104:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 167 base pairs  
(B) TYPE: nucleic acid  
10 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :104:

CTTATGATTA ACTAAGCAAA TCTTTCATAG AAAGATATTA TCAAAGCTGA 50  
AGAAATGCAA ACTTNAACAA AGTGCCGTGA GATTCCGGAA AAACCCTTAA 100  
20 CCGATTGAAT GGTTTTTTTAA GAATAAAAAA GAAGTCTGAT ACTGAACTAC 150  
AAGTCGCAAG GAACATC 167

25 (2) INFORMATION FOR SEQ ID :105:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 122 base pairs  
(B) TYPE: nucleic acid  
30 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :105:

TATCTGCATA TCTAAACATA GAAAAGCACA ATAAAAACAC ATATCATAAC 50  
CTCACGGGAC CACCATCATA CAGCAATTTG TCATGATCAA AAGAAACATC 100  
40 ATTAGTCGTG CCATAACTGT AT 122

72

## (2) INFORMATION FOR SEQ ID :106:

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 255 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :106:

GAATTCTTCA CTCCAGATTT CCAATGCCAA GATACATTGA TACTGAACAT 50  
15 GGAGGCAACC AGGCCCGTTT CCTCCTTTCA AAGTCAACC TCACAGACTC 100  
ATAATAATAT GCATGCCTGG GGGCAGGAGT CTGGAGCACC TATTCTNACA 150  
GATGATGTTA TTTACAAGTG TTTATGGATC ACTTGAAGAA ACTTGCTGTG 200  
20 TCCAGTGCTG CTTGAAGTGC TAATAATGTT AAAGACACTT AAGAAGATGA 250  
AATAA 255

25

## (2) INFORMATION FOR SEQ ID :107:

## (i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 227 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

## (xi) SEQUENCE DESCRIPTION: SEQ ID :107:

GGACGTGAAT TGGTGAATA TTTACAAAGA AACTGTTTT CTCAAAACAC 50  
TGTTCAATTGG TTGCAAGAAT GAATACTGAC TTCAGAACTC AAACAATGGA 100  
40 AGAACTTGCA TTTTATGGA ACTCAGTATT AAAAGAAAAT ATAATGTGAT 150

AGCACTTTGC AGATATGTCT AGACTGTGAT CTGAAGCATC GTAGTTTCCT 200

ATACCAAGAN ACANTTATGT GGTAAT 227

5 (2) INFORMATION FOR SEQ ID :108:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 162 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :108:

GAAAAATNGC ATGAAAGAAG ACTCTNNNN NGCCATACCA TGGTACAATA 50

ATCATNAAAA NACAANAACA AAAACAAACA CATAAAACCA CTCACATATA 100

20 CATGTAGATA CAACAACNAT ATAATATCAA TAAAAAAAAA ATAGNAAAAA 150

AAAAAATAA CA 162

25 (2) INFORMATION FOR SEQ ID :109:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 154 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :109:

AATTAAAAAT ATTAAACAAA ACTACCACTC CTCCTTATTA AAGCCCATAA 50

AAATAAAAAA CGAAACCCGA GAACCAAAAT GAACGAAAAT CTTTCGCTTC 100

40 ATTCATCGTC CCCACAATNC CAGGCCTACC CCCCATACTG ATCATTCATT 150

GTTT

154

## (2) INFORMATION FOR SEQ ID :110:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 182 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
10 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :110:

15 ATGTGCCAAG TAAAAAATCA ATNGTNGCC TTTTCCATT NCGCGGACAC 50  
CCATAGGCAC CAAAAAAGG TGCTAATAAG TAACATGTTT TAAGATGCAG 100  
AATAAGCTAT GGAAACAAGG AATGCTCCAA GTGTCCCAGT CTTTCTCCTT 150  
20 GCACTCCTTG TTAATAACAA TACACTATAT CA 182

## (2) INFORMATION FOR SEQ ID :111:

- 25 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 94 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
30 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :111:

35 GAAGGTGAGA ATAGGGTAGG GGAAACAGTA GGACAGGAAG TATTCACGTA 50  
CNTCAAAACC AATGGTAGAA CATCACATTT CAAACTGCAA ACCA 94

## (2) INFORMATION FOR SEQ ID :112:

- 40 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 92 base pairs

75

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :112:

10 TAGGGCAGTG AAACCTAATC TGCCTGATGC TATAANTGAN TGAATTACAT 50  
GNTCATTNGT TAAATTTTGT TCTAAACCCA TTAGGAAATT GT 92

(2) INFORMATION FOR SEQ ID :113:

15

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 152 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :113:

25 GATTGTTTTT GCATTGCGTG TGTCACACAG CAGCACAAAG ACAATATATG 50  
TAAGCGTNNA TACACCAGAT TTGACACAAG AGATAGCGAA CACCACAAAG 100  
ATTAGGACAG ACCGCGTATA GTAGCTCTGA GGAACTCCAA GAATCTAGAG 150  
30 GG 152

(2) INFORMATION FOR SEQ ID :114:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 182 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

76

(xi) SEQUENCE DESCRIPTION: SEQ ID :114:

TTGGCACTGA CATCCAGGAC AACAAATGCA GCTGGCTGGT GGTTTCAGTG 50  
5 TCTGCAACGG GCCACTCCAG AACAGTACCA ATCCTGAAGG AAAATACNTG 100  
GCAGAAGGAG GCTGAGAAAG TGGCTCCGTG AAGGCNCTAT AGAGGGCTGA 150  
TCTGCCAGCA TGTCTTCAAT ATGAGGAAGG CA 182

10

(2) INFORMATION FOR SEQ ID :115:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 182 base pairs  
15 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :115:

GGCACTGACA TCCAGGACAA CAAATGCAGC TGGCTGGTGG TTTCAGTGTC 50  
25 TGCAACGGGC CACTCCAGAA CAGTACCAAT CCTGAAGGAA AATACNTGGC 100  
AGAAGGAGGC TGAGAAAGTG GCTCCGTGAA GGCNCTATAG AGGGCTGATC 150  
TGCCAGCATG TCTTCAATAT GAGGAAGGCA NT 182

30

(2) INFORMATION FOR SEQ ID :116:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 227 base pairs  
35 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :116:

77

GAGGTTCTTG AATATGTATT TTTTACTGAA AAAATCATTC ATAAANTAAC 50  
ATACAAAAAT GTACAAACAC ATGAGTAAAT AATGTAATGA CAAAGGACTA 100  
5 TTTTCGGAAA AGTGTTTTTT AAAACANNCT AGATTTCAGT GCAAAAATGT 150  
ACCCCTGGCA CCTCTTAAAA CGTAAGAGCA AGCTCAAAAA CACGTAGTGA 200  
TGGAAATAAG CTAGCTACGC TCAATGC 227

10

(2) INFORMATION FOR SEQ ID :117:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 172 base pairs  
15 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :117:

CGAGAGATTG GTAATGAGGA AGCAATTGG AGGGGNGGAA GCTACAANGA 50  
25 NNNNGGGAAT TACAACAATC AGTCTTCAAA TTTTGGACCC ATGAAGGGAG 100  
GAAATTTTGG AGGCAGAAGC TCTGGCCCCT ATGGCGGTGG AGGCCAATAC 150  
TTGCAAAACC ACGAAACCAG GT 172

30

(2) INFORMATION FOR SEQ ID :118:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 210 base pairs  
35 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :118:

78

AATGATGGAA GCAATTTTGG AGGTGGTGGA AGCTACAATG ATTTTGAAT 50  
TACAACAATA GTCTTCAAAT NNGGACCCAT GAAGGGAGGA AATTTTGGAG 100  
5 GCAGAAGCTC TGCCCCTATG NCGTGGAGGC CAATACTTTG CAAAACCACG 150  
AAACCAAGGT GGCTATGGCG GTTCCAGCAG CAGCAGTAGC TATGGCAGTG 200  
GCAGAAGATT 210

10

(2) INFORMATION FOR SEQ ID :119:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 95 base pairs  
15 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :119:

GGTAAACACA AAGAGTTTCT GATAGTGTCT GCACAACAGC AAACCAACAT 50  
25 TTGGTGAGGA ATTAGCAATT TCTTGCCAAA GAAATTGAT TCTGC 95

(2) INFORMATION FOR SEQ ID :120:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 168 base pairs  
30 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :120:

GGAGTATTTN AANNTTTC AA ACTTTATTAC TTAATGAAAC AGTTTCTATA 50  
40 TACTGCTTCC AATATACTTT AATCCTTTTT TTCTCGTTAA ATTTTCTTTG 100

79

TTGTTCTTCA GTTGAGCTGA GATACTTTTA ATTACTTTTT ATTAAGTCT 150  
TCCAGAAACC GTAACAGG 168

5 (2) INFORMATION FOR SEQ ID :121:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 231 base pairs  
(B) TYPE: nucleic acid  
10 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :121:

GGAGTATTTA TCTTTCAAAC TCCNTACTNA GTGAAACAGT TTCTATACCA 50  
CTGCTTCCAA TTACTANCTN TTTTNTCNGT TAAATTTTCN NCTGTTTTTC 100  
20 AGTTGAGCTG AGATACTTTT AATATNNNGT NACTGCTTCC AGAAACCGTA 150  
ACAGGTGCAG GAATAATTGA TGATATCCAA GTAGAGGCTG ATGNCAGCTA 200  
25 ATACATACTT CGGTGACNTT ATGCATCATG A 231

(2) INFORMATION FOR SEQ ID :122:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 174 base pairs  
30 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :122:

TCTATGGCAT GAATGTTTGC AACCAACNNN NNGGAAAGCC TTAAAGGAAT 50  
40 AGCTGTTCAC ATAGGAGACC GTGACAATGC TGTACGCAAT GCTGCACTAG 100

80

ACACCATTGT ACGGTGTACA ATGTCATGGG ATCAGGTGTT CAAACTGATT 150

GGAATCTTTC TGAAAAGGAT ATGA 174

5 (2) INFORMATION FOR SEQ ID :123:

(i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 170 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :123:

CTNNACAGGA GAAGNAAGTA ATGATCATTC CCCAAAAATG TTCTGTTATC 50

AACTGNNTTT ATAAAAAATC GATTGTGGGT AGAAGCAGAG AAAAGGCACT 100

20 TAGTAAAGAT ACTACATGAN GAAAAANNTC TGCCCTTTGA ATTCTTANGA 150

AACATNNTNG NNGAATCAAT 170

25 (2) INFORMATION FOR SEQ ID :124:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 157 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :124:

AAGTAATGAT CATTCCCCAA AAATGTTCTG TTATCAACTG NNTTTATAAA 50

AAATCGATTG TGGGTAGAAG CAGAGAAAAG GCACTTAGTA AAGATACTAC 100

40 ATGANGAAAA ANNTCTGCCC TTTGAATTCT TANGAAACAT NNTNGNNGAA 150

81

TCAATNT

157

## (2) INFORMATION FOR SEQ ID :125:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 169 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :125:

15 CAACTTGAAA TACATTATGA TGTCTGATAT GATTAAATAT CATTGAGNAT 50  
CTTGCAAACA AAAAAAGCAA AAAATTAAAT CTCCATATCA ATCTTAAATT 100  
CTTGGCATAT TTACTTCTGG TAAATATTAC TTCTGGTCCT TATTCTATAT 150  
20 GTGTTATTGA AATTGTGTT 169

## (2) INFORMATION FOR SEQ ID :126:

- 25 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 90 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :126:

35 GTTNGTTNN NNNNTGTTCC ACCTTTTGTT GAATTTTAGT TGTTAGGCTG 50  
AACCTCCGAG CAGTTTNAGG ACTTGCCTGA GTTTTCTTC 90

## (2) INFORMATION FOR SEQ ID :127:

40

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 160 base pairs

82

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :127:

TTTAGTTTAC TTCTGTTCCA CCTTTTATTG AAATATTAGT TGTTAGGCTG	50
AAAGCCTCCA GTTAAGAACT TGCTGAGTTT TTTTGTTTCAG CAACTTGACA	100
TTTACTATGC GCATTATATA NCTCAATTAT GTCTGTTTTT TATGCTAAGT	150
AGGAAAACCA	160

## (2) INFORMATION FOR SEQ ID :128:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID :128:

GCCCACAACT TACATCCTCA TTATTGGCGC CTACAACTC AACTACGAAC	50
ACACTCACAG TCGCATCATA ATCTTTTGAG GACTTCAAAC TTACTCGGCT	100
ACCGCTTTTT GATGACTTCT AGCAAGCCTC GCTAACCTCC CTTACCCCCC	150

## (2) INFORMATION FOR SEQ ID :129:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 182 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40

## (xi) SEQUENCE DESCRIPTION: SEQ ID :129:

5 AGAGAGACAG ACACCATGGA GCCACAGGGG CAAGAGGNNG NTTTCCGAAG 50  
CAGGGGANNG GCTATCACTC GGACGGACCN NNGCTCAACG AGTCCCACGA 100  
GAACACACCA GAAATTTGTC ATTGCACTCA ACCAAAATCG ATATCAGCAA 150  
10 TGAAAAACCC AAAACAGTTA CGANGCTAAT CC 182

## (2) INFORMATION FOR SEQ ID :130:

## (i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 219 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID :130:

GGACCATTCT GATCATCCTC ACTGGACGCC ACAGGGGCAA GAGGGTGGTT 50  
25 TTCCTGAAGC AGCTGGCTAG TGGCTTATTA CTGTGACTGG ACCTCTGGTC 100  
TCAATCGAGT TCCTCTACGA AGAACACACC AGAAATTGT CATTGCCACT 150  
30 TCAACCAAAA TCGATATCAG CAATGTAAAA ATCCCAAAAC ATNTTACCGA 200  
TGCTTACTTC AAGAAGAAG 219

## (2) INFORMATION FOR SEQ ID :131:

35

## (i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 181 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

84

(xi) SEQUENCE DESCRIPTION: SEQ ID :131:

5 AATAATTCAT CCACTTATGG AGGAGGAGGA GAATGTGGAA GAGGTAAAAA 50  
GCTGGGCACA AGTTCATATG CCTATGAGTC AGTAAAGACT GAAGTAATGT 100  
CCTATGTTGA GCTGGTTATT TTGATATATG ATAATAATTA TCTTTGTAGT 150  
AGAACATCGT TAACGGAATC ACAGATATAT C 181

10

(2) INFORMATION FOR SEQ ID :132:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 188 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :132:

GACCAGCAGC TGTGGACATT ATGAGAAAGT GAAACCTGAG ATCCNCTGTT 50  
25 GATTGAGAAA TGCAACACCT CAAAATGNGG GACAGCTCCT GATTACCAGG 100  
TAGAAGATGN AAACAACTGG GGTGTCCATT CAGGAGGAAA CAATTGCAAG 150  
CTAAGAACTG TTGAGAGTGA AGCTGCATTT TCTGNACC 188

30

(2) INFORMATION FOR SEQ ID :133:

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 190 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :133:

85

GAGGTTGGGT CGTTGCATCC ATCATCAGGA GTTGACTTGT TCTGAGCAAC 50  
TGAACAGAAC ACACCGCGAT GCTCTCGACA CTCCGCTCCT GGACTTCAGT 100  
5 CACGAGTGAG TTGATGGTGA CTTGACCTGA GAGATTTTAC AGAAGCTCTG 150  
TGAAGTTGGT GTGGAAGAAA TCTGAACTGT TCAAGTTAAC 190

(2) INFORMATION FOR SEQ ID :134:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 235 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

15

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :134:

20

ACATTACGAT CACTGATAGT TGGTGTGCGA CTGAAACCCA CATNTTGGTC 50  
AATCTCCTCG TAGAGCTTCT TCTTACCTG AGGATTGGCA GCAGGAAGGC 100  
25 CAGGGTCCAT TTAATAAGA GGTGGTGATC TCCACGCCAG CCCCAAAGAT 150  
GTCCCTATA TGGTGAGAAT GNGTCATCTG AAAGCAGCTC TGAGTCTTGA 200  
TCTGGGCCAG CATTGCCATT ATTGAGTTTA TCTAG 235

30

(2) INFORMATION FOR SEQ ID :135:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 147 base pairs

35

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :135:

86

GAGAAACAGT ACCATCCANG ACACGATGTG GTGGAGGTTG ACNCCGCTGT 50  
 ACCCCAGAGG AGCNCCACCT GTCCAAGATG CAGCAGAACA CTACAAAATC 100  
 5 AACTATGTTT TTTAGCAGAT GCAGGACTAG ACCCCCACGC AGCTCTG 147

(2) INFORMATION FOR SEQ ID :136:

(i) SEQUENCE CHARACTERISTICS:  
 10 (A) LENGTH: 171 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :136:

GAAAAATGNG TTGANCCATT CATCCACAAA TTGACTTGCC TGAACAACCA 50  
 20 CCAAACAATA CACTAATGNT TCACACNTTT NCTTTTACTT GNACNTTAAG 100  
 NTCCCANTGA GTCACGGTGA CTTACCCTAA ACATCTCAAN NGTNNTCTGA 150  
 25 CTNAGAATGC GGAGGAGATC T 171

(2) INFORMATION FOR SEQ ID :137:

(i) SEQUENCE CHARACTERISTICS:  
 30 (A) LENGTH: 159 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :137:

ACATATATGT GGTAGGATAG AGAGATGGNN NNGTGTATG ACATAGGTGT 50  
 40 TTCTCGTGTG ATGAGGGTTT ATGTGTTATG TGGGGTGAGT GAGCCCATTG 100

87

TGTTGTGGTA ATATGTGAGG AGTATAGGCT GTGACTAGTA TGTTGAGTCT 150  
GTAAGTAGG 159

5 (2) INFORMATION FOR SEQ ID :138:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 179 base pairs  
(B) TYPE: nucleic acid  
10 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :138:

CCCACGACTT ACATCCTATN ACNCTTCGCC TAGCAAATA AACTACGAC 50  
NCACTCACAA TCGCTCATAA TCTCTNAGG ACTTCAAAT NTCTCTNTGA 100  
20 NCCTTTTGAT GACTTCTACA AGCCTCGCTA CCTCGCCTTA CCCNTGTNC 150  
TNCGGGAGAA CTCTCTGTGC TGTACCAGT 179

25 (2) INFORMATION FOR SEQ ID :139:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 177 base pairs  
(B) TYPE: nucleic acid  
30 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :139:

GACCTGGGAC GTAAATGATG AGACGGGTAC TTTGGCGGAC ATGAAGGAAC 50  
TGGCATATGG AACCTTGGCT GTGAAGCTGC AGACTATAAG ACAGCATGAG 100  
40 ACGACAATTC TGCTACTGCA ATGATGACAT CGTTTCAGAC CACAAAAAGA 150

88

AAGGCGATGA CCAGAGCCGC AAGGCNG

177

## (2) INFORMATION FOR SEQ ID :140:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 72 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :140:

15 GTTTACAACA TTTACATCCT ATGAACTCAT GGATTATAAA ACATTTGTGA 50  
CTTATACTGT CTNTGTCACT TA 72

## (2) INFORMATION FOR SEQ ID :141:

20

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 62 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID :141:

30

GTNGGCTGAA ATGAAANAAT AAAACCAAGA AACGAATTTA AGTATTNGTT 50  
TTAGTACGNA AA 62

35

## (2) INFORMATION FOR SEQ ID :142:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 127 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

## (xi) SEQUENCE DESCRIPTION: SEQ ID :142:

5 ACCAGTNNNT GATTGGTAAA TGGGAAATAT AATTGATTCT GATCACTCTT 50  
GGTCAGCTTC TCTTTCTTTA TCTTTCTTTC TCCTTTTTTA AGAAAACGAG 100  
TTAAGTTTAA CAGTTTGTCA TTACAGG 127

## 10 (2) INFORMATION FOR SEQ ID :143:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 198 base pairs  
(B) TYPE: nucleic acid  
15 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## 20 (xi) SEQUENCE DESCRIPTION: SEQ ID :143:

AATATAAAAG ACAGCAGTTT CACATTTTCAAC ATATTTGAAA AACATTTCAA 50  
AACCCTCTAA TAAGTATTTA ATGAAAATAA ATTTATCGAA GAGAAACAAT 100  
25 GACCACAAAA TTAATACTAC CAAATCATTG CTGAGACTTT TTGCATTACA 150  
ATATTTGGAG AGTAGGTGAA GAAAATATAG AACAGAACAT GNACATTT 198

## 30 (2) INFORMATION FOR SEQ ID :144:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 174 base pairs  
(B) TYPE: nucleic acid  
35 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## 40 (xi) SEQUENCE DESCRIPTION: SEQ ID :144:

GTTTCTCTNT ACGTCATCCA CCTTGACATG ATGGGTCAGA AACAAATGGA 50

90

AATCCAGAGN CAAGTCCTCC AGGGTTGCAC CAGGGNNTAC CTAAAGCTTG 100  
TTGCCTTTTC TTGTGCTGTT TATGCGTGTA GAGCACTCAA GAAAGTTCTG 150  
5 AAAGTCTTT GTATCTGCTT TGNA 174

## (2) INFORMATION FOR SEQ ID :145:

(i) SEQUENCE CHARACTERISTICS:  
10 (A) LENGTH: 156 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

## (xi) SEQUENCE DESCRIPTION: SEQ ID :145:

GAGAAATAGT ACTTTAAAAT AAAACTAACA TGGTTTGATC AGCTTGAAAT 50  
20 AAGATTCATA AAATGTACCT TTTTGTATTG TTTTGTCTN GAGTTTTCGA 100  
TTGAGANCAT TTGGTAAAGA TAAAGAGGTT TCCTGGGTGG CAAAAAATTA 150  
25 TTTTGG 156

## (2) INFORMATION FOR SEQ ID :146:

(i) SEQUENCE CHARACTERISTICS:  
30 (A) LENGTH: 151 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

## (xi) SEQUENCE DESCRIPTION: SEQ ID :146:

AAGATTCNNN NNTCCATTGA ATGTTACCTG TGCCAGAATT AGAAAAGGGG 50  
40 GTTGGAATTT GGCTGTTTTG TTAAATATA TCTTTTAGTG TGCTTTAAAG 100

91

TAGATAGTAT ACTTTACATT TATAAAAAAA ATCAAATTTT GTTCTTTAAT 150

T 151

5 (2) INFORMATION FOR SEQ ID :147:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 177 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :147:

CTTTATTTTT CTTATACAGA TTCAGAGAAG TAAAANNCAG TACCAAATC 50

CAGGTAANNT GGTTCGATCT GATCGATTG GCTGCATACT TTCGGTACGT 100

20 ATAACATTCT AACTTAAAA TAGAAATTTT TATATTACAA AACGAGGAAG 150

TAAAATTTTA AAAGTTAAAG TACTAGC 177

25 (2) INFORMATION FOR SEQ ID :148:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 148 base pairs

(B) TYPE: nucleic acid

30 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :148:

GATTCNNNNN TCCATTGAAT GTTACCTGTG CCAGAATTAG AAAAGGGGGT 50

TGGAAATTGG CTGTTTGTG AAAATATATC TTTTAGTGTG CTTTAAAGTA 100

40 GATAGTATAC TTTACATTTA TAAAAAAAT CAAATTTTGT TCTTTAAT 148

## (2) INFORMATION FOR SEQ ID :149:

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 204 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :149:

AGATTCNNNN NTGGNATTGA ATGTTACCTG TGCCAGAATT AGAAAAGGGG 50  
15 GTTGGAATT GGCTGTTTTG TTAAATATA TCTTTTAGTG TGCTTTAAAG 100  
TAGATAGTAT ACTTTACATT TATAAAAAAA ATCAAATTTT GTTCTTTATT 150  
TTGTGTGTGC CTGTGATGTT TTTCTAGAGT GAATTATAGT ATTGACGTGA 200  
20 ATCC 204

## (2) INFORMATION FOR SEQ ID :150:

25

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :150:

35 AACATCGAGG TCGTAAACCC TATTGTTGAT ATGGATCTCT ATGAATAGGA 50  
TTGCGCTGTT ATCTCTAGGG AACCTCACCG TTGGCAAGTT ATT 93

## (2) INFORMATION FOR SEQ ID :151:

40

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 151 base pairs

93

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :151:

10 AATCGAGAGA AAAAATGATG ACACTGTAGC AATATCGTCG GANTCCACCT 50  
ACTTTGGGAT CAGCCTATCC ATCCGTGTCT TCCTATTTAA ATCGTCTATC 100  
CTCTATCCTT CCCCTGTCTT TTTNTGAAAA GGAAAAAAC CAGGAAGGTG 150  
15 T 151

## (2) INFORMATION FOR SEQ ID :152:

## (i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 109 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID :152:

30 TCTGAGAGGA ATACTNNTAA GTGCAATGAA TATTGCAAAT TTTCCCCCCT 50  
CTAAGTAATT CCCGATATTA GCAAANCANN NANATTAATG TCCCAGTGAA 100  
TGTAGCCTC 109

## 35 (2) INFORMATION FOR SEQ ID :153:

## (i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 136 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :153:

5 AAAATTATTT TCACAGTCCC CCCCAACTCT CATTGCGTCG TTAAAGTCCC 50  
TCCAATCCTT TTTTAGTTGT GAAAAAATAA GGGGCCTTTA AAGGAGGAGG 100  
AGGAAAAGGG GAAAAAACC CATAATGGGC CTAAAA 136

## 10 (2) INFORMATION FOR SEQ ID :154:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 160 base pairs  
(B) TYPE: nucleic acid  
15 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## 20 (xi) SEQUENCE DESCRIPTION: SEQ ID :154:

CATCTTCATC ACCATCACAA TACTCATCAT CACCACCCTT CATNCACTAT 50  
CATCTTCTAT GACTGCAAAC TTCTTATCTT TCTCTTCATT ATAGAAAGTT 100  
25 TCAAGATGAG TATACGCATC TATCATTCGA ATTGTGTCAT TAATTTGTAG 150  
GGCCTCATTG 160

## 30 (2) INFORMATION FOR SEQ ID :155:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 191 base pairs  
(B) TYPE: nucleic acid  
35 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## 40 (xi) SEQUENCE DESCRIPTION: SEQ ID :155:

ACCAGTNNNN NNNGGTCAAA TAGGGAAATA TAATTCGATC TCTCGAATCA 50

95

ACTCTCTGGG TCAGCTTTCT NCTTNTCTTC TATCTTTNCT TNTCTCCTTT 100

TTTTAAGAAA AACGAGTTAA GTCTTAACAG TTCTCGCATT ACAGGCTTGT 150

5 GACTTCATGC TTAGTGTAAG GTGGAAGTTG AGATATTTTA A 191

(2) INFORMATION FOR SEQ ID :156:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 139 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :156:

CAACTGAACG CTTTGGTCAG GCTGCTACAA TGGAAGGAAT TGNGGGCNAN 50

20

TTGGTGGAAC TCCTCCTGCN NTCAACCGTG CAGCTCCTGG AGCTGAATTT 100

GCCCCAAACA AACGTCGCGG ATACTAATAA GTTGCAAGTG 139

25

(2) INFORMATION FOR SEQ ID :157:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 172 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :157:

GGTACAGAGC ACTCTGTACC AACACACAGA ATTTACTGTT CTGCAAATGA 50

CCAATACTAA AAATTTATAA AGATGTGCAC AATTNNNNGC AGGCAATCTT 100

40

TCTTTTGTTT ACAAGATACA ACATTTAACA GTTATTAAAT GTAATCCTGA 150

96

AGCACCCGCA AATTACCTT TG

172

## (2) INFORMATION FOR SEQ ID :158:

5

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 93 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :158:

15

GGGTGGCTGT TNNGTATATC TCGTTAGTAA ATGTACATGC TCTTCAGGTT

50

CTAGGGCTCC TGTTAGGGGA GGGAGAAATG TTGGAAGNGG GGG

93

## (2) INFORMATION FOR SEQ ID :159:

20

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 102 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

25

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :159:

30

GNATTTTTTT ATTGATATAT CATAGTTGTA CAAACATTG GGAGTNCANG

50

TNGATACTTT GATACTATCG TGTNNNNNGG ATAATCACCA AATTGGATTC

100

35

CA

102

## (2) INFORMATION FOR SEQ ID :160:

40

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 205 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

97

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :160:

GCTTTTNNNN NNNNNNNNNC AGGTTTATAT TTACAATAAT TATCTTCCTA 50  
TAGAAGCAAT AANNCNAGTA TTCTCCAGTA ACAACACANN NNNATATTCT 100  
10 ACTCATCAGA GTTGGGAAAA ATAGGAATAA AGCAGATTCC ATACAGAAAT 150  
ACCGTACTCT GCATATGTAC AAATAAATTC AATATATTAA ATCATTTTGA 200  
15 GCGGA 205

(2) INFORMATION FOR SEQ ID :161:

(i) SEQUENCE CHARACTERISTICS:  
20 (A) LENGTH: 150 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :161:

AACTTTTTTA ATGGGTCTCA AAATCTCTGA GACAAAATTA CTNNGNNNAA 50  
30 AGTTGTTTTTC CATATAAAAA ANNNNNNTGA TTTTAAAAA ACTAANNAAC 100  
TTAAAAACNT GCCACACGCA AAAAAAGAAA CCAAAGTGG GNCACCAAAA 150

35 (2) INFORMATION FOR SEQ ID :162:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 77 base pairs  
(B) TYPE: nucleic acid  
40 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :162:

5 TATTCAAAG AAAACATGG GTAAAAATGA TAGTGTTAA TCTTGGCTCT 50  
GTGTACATAG ATAGATACCT GTTACAG 77

## (2) INFORMATION FOR SEQ ID :163:

10 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 182 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear  
15

## (xi) SEQUENCE DESCRIPTION: SEQ ID :163:

20 GAAAATTATT TTCACATCCC CCCCAACTTC TTGCTCTTAA TCCTCATCTT 50  
TTAGTTGAAG AATAAGGCTT AAGAGAGAGA AAGGAAAAC CATAATGGCT 100  
AACTTAGCAG CACAACACGG TTCTTTTATC AAGGCGTNAT CATCATTTCT 150  
25 CAAACTGACA TGCTACAGAA ATGTCTTCCA AA 182

## (2) INFORMATION FOR SEQ ID :164:

30 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 182 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear  
35

## (xi) SEQUENCE DESCRIPTION: SEQ ID :164:

40 GAGGGAGCAA AGAGAGCCAT AAAGGCTCGT GCTGGGAAAG AAAGCTGTTA 50  
TGCTTAGACT TCTCTAGGTG AACTCAGAGT CTTCAAAGAG GAAATGTTAC 100

AAATTGTCAC CCGCCAGCTT TCTGGCCAGT AAGCAGAATG CCAGGTTGCT 150  
CAGATTCACA GACATTTGCA AAACAGAAGA TG 182

5 (2) INFORMATION FOR SEQ ID :165:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 119 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :165:

GTATCTCCCT CTACATCCCT CCCGAAATAC TAGGAATACT TATTCTATAT 50  
GAGACATATA TACCACCCAA GTTTTAACAC CATATCCCAT CGGCTGTTAG 100  
20 TGTATATAAA AAGAAATAA 119

(2) INFORMATION FOR SEQ ID :166:

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :166:

35 GTACAAAGCC ACTCATCCTC GTGTGCCTAT CACGTTTTCC AAACACATAG 50  
GATCCCATCT CAGGAGCAGG ACCAGTGTTT AGCTAGATTA AACTTCGCTG 100  
GTGATCTTGT TGATGCATAT AAAGTAATCT GGCATATATG GTTAAATTCA 150  
40 AGATGTTATG GCAGAAGTGA CTTGTTTTGC TCAACAAGCA TTG 193

100

## (2) INFORMATION FOR SEQ ID :167:

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 185 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :167:

GTTCTGACTN AGAACTGAGC ACATAGCATT GACGCGGTAC CCTTGGAGAG 50  
15 GGTGTGCTAG GAGGAGTGCT TGGCGAATTT GGACACGTAC TAATGTCTCT 100  
GAGCCAGTCT GAATCTCTGT GAAGATGCCC CAGTGGAGGT GGCTGAAGAT 150  
TAAATGGACA GTTATAAAG TGTCTGGP GCCGA 185

20

## (2) INFORMATION FOR SEQ ID :168:

## (i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 163 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :168:

GGACAACACA GCACCCATCC ACTACCCATT CAGAATTTAT ATAGAATATG 50  
35 TACCCATGAT TATCTAGGTG AATCAATGCA ACAGTAGCTC TGATGTCCAG 100  
ATTCCTAGT CTATTATTTT GTGTACAGAT CCTCTAACCA CTTAGAAATA 150  
ATTTTAAAA ATA 163

40

## (2) INFORMATION FOR SEQ ID :169:

101

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 202 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :169:

10

AGACAAATTC NNNNTNNNNN NTGCCTGATA ATTCAGATG CCACCGTATA 50  
GCAAAGGGTG AACATGTTTT CAACCCTTTA ACTTTTTACG GTGTTTGAAG 100  
ACCAGCTACT CCTTAATATT TATCAATGGA TTAAGAAGTT TAAGATTTTG 150  
CAGATTTACA ATTTGGGTTT TTGTCTGGAG TTGCTTCGGT TTGAAGCCCC 200  
CT 202

20

## (2) INFORMATION FOR SEQ ID :170:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 168 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :170:

TCAGGGAACC AAAAACTGG CTTGCTTGGC ACCCAGGGAC AGTAGCTGTT 50  
TGGCTCTCCA CCAATTAAA AAAACAAATC CCTGCCCTTT CCCCCACCCC 100  
ACTAGCTAAG CAAGAGCAGA GCTCTGATGA AGAGCCAGTG CCGGGTGCCT 150  
GGTGCCCAGG GCTGTAAA 168

40

## (2) INFORMATION FOR SEQ ID :171:

102

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :171:

10

AGAAGTCAAC TAAAGCTTCA ATGCATCAAT TTATAANGCC TCANAGATCA 50

GCAATTTATG ACACTTACAT TTACAGTCGA CCTTTACTAA CCAGGCAAAC 100

15

TTCCCGAAAT GATCAGGACT GATTCATCTC CTGAAATTNN CNGT 144

## (2) INFORMATION FOR SEQ ID :172:

## (i) SEQUENCE CHARACTERISTICS:

20

- (A) LENGTH: 91 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID :172:

30

ACCCACAGNN NNNACCTAGA GGGCCAGCGC CCAGAGAGGC ACGTAGAAAT 50

GGGGACAGCA CGTTTATAGA CCACCAGAAA TTGAAGAGGA A 91

## (2) INFORMATION FOR SEQ ID :173:

35

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 204 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

103

(xi) SEQUENCE DESCRIPTION: SEQ ID :173:

	GATTTTTTAA TGGGTNGCCT CTTTGTAGCTT GGAATATTAC GTTACTTTA	50
5	ATCCAAGTCT AGGCCTTTTA AAGGGTCCTT AAAATTAAAG TTCAGAATGT	100
	GAATCCCTTT GACATCTATT ACAGGTTATA GGACCTTTTT GGTGTGATTA	150
	CGGTTTTCAA TACGATTGTA TAAATGAAGT TAACTTGGCA GAAGTTAAAA	200
10	TGGA	204

(2) INFORMATION FOR SEQ ID :174:

15	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 241 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear
20	

(xi) SEQUENCE DESCRIPTION: SEQ ID :174:

25	GTAAATTTC A CTACATCTTT TNNTNTGACT TTCATGCATT TCTCATACAT	50
	TNNTNNCNGA TGCTTGACTT TATTGCTTCC TAGCAATAAT CTGCATTTAA	100
	ACGAAAGGCG GTTCAATTCA TCAACTTGAA ATGACTATTT ATTTTNNAGG	150
30	ATTTTTTAGG GGAAGAGTAC CCATTTCGTT TATAAAAACA GATGACAAAT	200
	TTCTTAAAGA AACAGAAGCA CAATACTTTC GAAATACAAC G	241

(2) INFORMATION FOR SEQ ID :175:

	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 211 base pairs
	(B) TYPE: nucleic acid
40	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :175:

5 GGTGGGCTCN NNNANNANNG TTCTACACTG TGGTATAAAC TTGTCGTGGT 50  
TCTCGTGATA GAAACAGAC ACTGACCTTG GGTATAGTGG GCCTATAAAT 100  
AACAAACCCT TGGGTACTCC TGAATAGGGG CAGGGCCCCC TGGGCCTCCC 150  
10 TTACAGGTTT CTTCAGGGAA ATGGTCCCTG GGATAATTCT TTAGGGCCCT 200  
TTGGCCCTTT T 211

## (2) INFORMATION FOR SEQ ID :176:

15

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 252 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
20 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :176:

25

AAAATAAGAA TAAACATCCA TAATAGTNAT AGATANATCC NTTTATTTAG 50  
NACATCAGCA ACGACTGCTT CACACCAAAT CCCTTCCTCT GNGAATGATN 100  
30 TATATAACTC TAGTACTGCT TTCCATGAAG AACCTTGCAA ATTGATTGAA 150  
AGTCCAGGAT NNCTCGCTAA TCCTCCACCA TAAGATTTCT GACCTATGAT 200  
AACTCCAAGG TGGCAAACAG AGAAATCAAC TTCCTTATAA ANAAATCCNA 250  
35 AT 252

## (2) INFORMATION FOR SEQ ID :177:

40

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 279 base pairs  
(B) TYPE: nucleic acid

105

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :177:

	GCGGGCGACT TTCCATCCCT CGAACCAAGG CATGTTAGCA CTTGNCTCCA	50
10	GCATGTTGTC ACCATTCCAA CCAGAAATAG CACAAATGCT ACTGCGCGAG	100
	TTGCAGCCAA TCTTCTCAAA GCAAACCGAC TTCCTAACAA CTNTCTACAT	150
	CTGGCTCGCT GCAGGCGACT CAATGAAATC CATCTTTAAC ACCACAATCA	200
15	TTGTTTNACA CCCAGTGTGC AAGCCAGGAG GGCATGTTCT GAGTCTNTCC	250
	ATCTGAAGAT ACCAGCTTCA AATACTAAT	279

20 (2) INFORMATION FOR SEQ ID :178:

(i) SEQUENCE CHARACTERISTICS:

	(A) LENGTH: 157 base pairs
	(B) TYPE: nucleic acid
25	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID :178:

	TATGCCCTGA AATGAAACCT CTAAGTTTGA CAAAATACCC AAAAAACAG	50
	ACCTTCCTNG TTAACACTTT ATAAGAAGGT GTGACATTG GTGGGTGGTC	100
35	GTTCTCAATT TATAAANAA TAAATGACTT TAAAGGAGAA ATAAATTTAT	150
	GTCAGGA	157

40 (2) INFORMATION FOR SEQ ID :179:

(i) SEQUENCE CHARACTERISTICS:

106

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :179:

10 GATAATGCAA CTTTGGACAG GAAAGCGCGA TTTTACTAT 39

(2) INFORMATION FOR SEQ ID :180:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 157 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :180:

25 GCAAAC TCAA ACTACGGACG CACTCACAAT CGCTCATAAT CCTCTCTAAG 50

GA CT TAAACT CTACTACACT AATACTTTTT GATGACTTCT AAC AAGCCTC 100

GCTAACCTCC CTTACCCCCC ACTATTAACA CGGGAGAACT CTCTGTCTAG 150

30 TACCACA 157

(2) INFORMATION FOR SEQ ID :181:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 195 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :181:

107

CCATCCAGGC CAAATAAGCN CCGGCTATGC CCNTGTATTG GATTGCCACA 50  
CGNCTCACAT TGCATGCAAT TTGCTGAGCT GAAGGAAAAG ATTGATCNCC 100  
5 ATTCTGGTAA AACTGGAAG ATGACCCTAA ATTTTGAAGT TGATGATGTG 150  
CCATGTGATA TGGTTCTGAC AAACCCATGT GCGTTGAGAG CTTTT 195

## (2) INFORMATION FOR SEQ ID :182:

10

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 146 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 15 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :182:

20

CATGGTCTTA ACCAGTGTC A GATGGAATCA GTGGATAAAT CCCCAGGTTT 50  
GTTTGTCTT CAAATGGGAC AATTTGAGGA ATGCTTTAGG CAGAGGACTC 100  
25 AGATGACAGA GCGCCAACCA CCCACAATAG AAACCTGCTC ATCACA 146

## (2) INFORMATION FOR SEQ ID :183:

## (i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

## (xi) SEQUENCE DESCRIPTION: SEQ ID :183:

TAGAGGAATA GGGNNNGNGA CGCCCCNAGT TGTAGGGACG GACGGAGGAC 50

40

## (2) INFORMATION FOR SEQ ID :184:

108

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 248 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :184:

10

ACGNTTACGG TCACTGATAG TTGATGTGCN NCTGAAACCC ACATCCGATC 50

AATCTCCTCA TAGAGCTTCT TCTTCACCTG AGGATTGCGC AACAGGAAGG 100

15

CCAGGATCCA TTTACCACAG AGGCGGGATC TCCACGCCAA CCCCAAAGAT 150

GTCCCCTATG ACGACGAGAA TGTGATTATC TGAAAGCAAC TTGATCTTGA 200

TCTGGGCCAG CATGCCTCAT CTGATTCATC TCGCTTCCAT CAATGNGT 248

20

## (2) INFORMATION FOR SEQ ID :185:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 113 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

25

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :186:

AATGATGAGT AAAAGATTCA ACAACTCACA GCCCTGGGGG CACTCAGGCT 50

35

ACTGCTAAGG CCTGAGAGTT TTGCAAAAAT GCGCAGAGAA ACACCCTTTG 100

AACGTGGCTT TCT 113

## (2) INFORMATION FOR SEQ ID :186:

40

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 148 base pairs

109

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :186:

GGGCCCCCTG ATCAATTCTT TGGATGCTTT TCAAATTTCC CAGGATCCCG 50  
10 ATGTCGTCAT ACACTCCGAA CATGACCCTT TTTTCTTCCA ACGATCAACC 100  
ACTNCGNGGG ACGGGAGAGT GAGCCTTATA CCGATCAATC TGCACACC 148

15

(2) INFORMATION FOR SEQ ID :187:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 248 base pairs  
(B) TYPE: nucleic acid  
20 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :187:

TCCTTACTGT AAGAGCCATT TAAACGATTA AAATCCCACT NGCCATACCG 50  
TAAGATGATA GGACCAACCA TACCTACCGA TCAAAAATTT ATCAATCCAA 100  
30 GCCAACTACA CTCCCACTGC TAAAAAGATG AAAGGACCAA TCAAAGATTT 150  
AATTAACTA AAGGGAAAGA ATCAGAGACA GAGAATGAAG AAAGAAATTC 200  
35 TAAGTTGCGA CGGACAAACC AGAACAGACA ATGAAGCCTT TCAACTGC 248

(2) INFORMATION FOR SEQ ID :188:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 146 base pairs  
(B) TYPE: nucleic acid  
40 (C) STRANDEDNESS: double

110

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :188:

TATGAAGAAG TGCAGCACTG GCCAACACCA GGGTTTACTG AATCATTTC A 50

GTTTAATACA TAAGTGTC AATAATGT CAACCCTCCC TCGCCACAGC 100

10

CAATAATTTG TCCTCACTGA GTTGGCAACA AGTGACTGCT GTGACT 146

(2) INFORMATION FOR SEQ ID :189:

15 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 81 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :189:

25 ATTTACCACA AGGGACGATT TCCACACCAA CCCCCAAAAT GTCCCCTATG 50

ACGACGAAAT GTGTATTGTA AACAGCTCTG A 81

(2) INFORMATION FOR SEQ ID :190:

30

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 136 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

35

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :190:

40

AAGTACAGCA TCCTGCTGCA AAAATGATTG TAATGNCTTC TCATATGCAA 50

111

GAGCAAGAAT TGAAGATGCA CAACTTCGT TCTGAATTTG TGAGCTTCCT 100  
GGATCAACTG AAGAACTTCT GAGGATTGAC CTGTCA 136

5 (2) INFORMATION FOR SEQ ID :191:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 152 base pairs  
(B) TYPE: nucleic acid  
10 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :191:

AGGATTTAAG ATGGGGACAG ACTGGTGAAA ATGCGGCTGA CTGGAAGGAA 50  
ATGGGGCATA CGAGTAATAT GTACATATCA AACAATCAAT TGCCTCCTGA 100  
20 AATCAAAAAA TCAAATGGTG AAATGGAGCC TCCTTGATAG TTAGGCCAA 150  
CA 152

25 (2) INFORMATION FOR SEQ ID :192:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 65 base pairs  
(B) TYPE: nucleic acid  
30 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :192:

TAAGCGAGGN NGTCTTTGAT TGCCTAGTAA GGTAAGACG ATTTTATAGA 50  
ATNAAGGTGA TTCCT 65

40

(2) INFORMATION FOR SEQ ID :193:

112

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2 ? base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :193:

10

AGGACCCAAA CTACCTTATT GCATTGAAG TTTTACTTAT NCTATTATAA 50  
TCTAAGAGCC CACCCAACAA GGCACACAC ATAGATGCTC ACACTCTATA 100  
GGCTGCCTGA TCCTGGACCA CCTGGGGCCC TGATTATGAT CTCCACGGGG 150  
CTGTCAATGA CTAGGGAAAG CTTTTTAAGA CCCAGCGATC ATGCAATGGC 200  
TCAACCATGG CGAATCAAAG TTAGCATAAT GTCCCAGCAA ACAATGTTA 249

20

## (2) INFORMATION FOR SEQ ID :194:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 194 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :194:

GGAAAGGGTG CCTCATCCCA GCAACCTATC CTTGTGGGNG ATGATCACTG 50  
TGCTGCTTGC NNCTCATGGC AGAGCATTCA TGCCACGATT TAGGTGAATC 100  
GCTGCATATG TGACTGTCAT GAGATCCTAC TAGATGATCC TGACTAGAAT 150  
GATAATTAAA AGTATTTACT TCGAAGCACC ATTTGAATGN TCAT 194

40

## (2) INFORMATION FOR SEQ ID :195:

113

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 121 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :195:

10 GTGATTTTAG TTTAAGGATA AGAAGCCACT ATATCAACGT CGGGGGGGTA 50  
TTTAAGTCAC ACACATAGTT AACAAACNCNC GTNGCGTGCA ATAAATACCA 100  
15 CATCCTTTNA TATGNNCNGN A 121

## (2) INFORMATION FOR SEQ ID :196:

## (i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 175 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID :196:

GGGCTTCNNN NNNNNNCATG TGCACTTAGA ACCGTTACTA ACCGAAACAC 50  
30 CATTTGCTTG TCAACAATGT ACCCTTGACA GCAGGGAGAA ACTTCTTTAT 100  
AGTCTCTGCT TCAGACAAGA TTACNGCTT TCTCCAAGGC CAGAGGCAAA 150  
35 TTGTGACCAC AAGTCTTGTT TCTTG 175

## (2) INFORMATION FOR SEQ ID :197:

## (i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 273 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double

114

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :197:

ACTGGCAACT TCTATGTACC TGCAGAACCC AAATTGACAT TTGTCATCAG 50  
AATCAGAGGT ATCAATGAAA TGAGCCCAA GGTTCGAAAG CTCGCAACTT 100  
10 CTTACCTTC ATCAAATCTT CAACGACCTT CGCAACTCAA CAAGCTTCTT 150  
ACAGTGAGGA TTGCAGAGCC TATATAGCTG ATACCCCAAT CTGAATCATA 200  
15 AATGACTAAT CTACAAGCNT GTTATGCAA ATAAATAAGA AACGACTTGC 250  
TTACAGATGC NTTTTAATTG TGG 273

20 (2) INFORMATION FOR SEQ ID :198:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
25 (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID :198:

GATTCCCCAA TAAGCAGACA CCTTGAACCA GCCTGGGGTG AGCGAAAGAT 50  
GNTATA 56

35 (2) INFORMATION FOR SEQ ID :199:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 base pairs  
(B) TYPE: nucleic acid  
40 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

115

(xi) SEQUENCE DESCRIPTION: SEQ ID :199:

5 GGACGCTGNN NNNNNNATCC TGCAATGCAC AGCACAGACC CCACCACAGG 50  
GGTTTTATCC AGCCCAAATG TCAACAGTGT CAAGTTTAAG CAACTCTTAC 100  
CGAGTGGGAC TCAATTCCCN AGTTGTATGG AA 132

10 (2) INFORMATION FOR SEQ ID :200:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 284 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID :200:

AAACTTTTTN GCACTTACAC AGACGAGACT TCACTGCNTG AGGATCATA 50  
GACATTTCAA TCGNACACAA ANTTAAAAA TAAACAAAT TTTAAAAAC 100  
25 CATNTTGAAT TTCCTTAAAA TTATTCCAAT ACTTTCCAAC TTAAATTCA 150  
GAACAAATCC TCCTAGAGAC TATCAATACC AATATCTTCA CATTGCTCAG 200  
30 CTGNTACATA CGNCCCACCA GTTCACAACT AATGACACAA CACTACATGN 250  
TCAAATCTTA TCTNNNATAG CACAGTAACA AAGT 284

(2) INFORMATION FOR SEQ ID :201:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 106 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
40 (D) TOPOLOGY: linear

116

## (xi) SEQUENCE DESCRIPTION: SEQ ID :201:

CCTGACACCA ATTCGCCCCA CATGTATGCG GGAAGAGGCC TGAGACTAGA 50  
 5 AGTCGTTGCC CTGTCCATCT CCCGGCCACA GGCTTCATTC CCAGATTNT 100  
 CTTGNT 106

## (2) INFORMATION FOR SEQ ID :202:

10

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 15 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :202:

20

CTTTGGA AAA CAAACATTTN TTATTACTGA AATAGCAAAA ATCATTCTAC 50  
 ACTCCTCCTA AGCATGTTCA ATTAGCATAC ATTCCAACAA TGCATGAAAA 100  
 25 AATTNCTAGC CAGAGGCATT TAAGTGATTT CTTCTAAGT GTTTGCTAAT 150  
 TCAATGCCAA GAACTATGAT GTTTATCNTT CTGATGGACA AATCAAGAAA 200  
 CAAAACAGAT ATAATACCAA GGGTAAAGCT GATATGACCC ACAACATTGT 250  
 30 CATTACTCTA ACTGTTAATC 270

## (2) INFORMATION FOR SEQ ID :203:

35

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 173 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 40 (D) TOPOLOGY: linear

117

(xi) SEQUENCE DESCRIPTION: SEQ ID :203:

AACTAAGGCA CATTGCCCTT TTTGACCTTT CTNNNGNACT ATTGAAATCA 50  
5 AGCTTATTGA TTAGGTGATA TTTTATAAC AATTGAAAGG GCAATATCAA 100  
ATAATGACAT ATGAGAATTT TTTATTACAT ATTAAAACTG ATTTTACTT 150  
TACAAAANNG NAATTTGCAA TTA 173

10

(2) INFORMATION FOR SEQ ID :204:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 164 base pairs  
15 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :204:

CTGCTTCACC ATCCTGGCGT CTACCAGCCT GGTGNGGCTG GGTACTGTGN 50  
25 ATCGTCTTCC TCAACAAATG CGAGACCTGC CAACCTGCAC TACACCACAT 100  
CCGCNCAAGA AGAAGAACCT GCTGCTTCAT ACAACACGGG GAGGCCCTGT 150  
CATTAACATT ANTT 164

30

(2) INFORMATION FOR SEQ ID :205:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 99 base pairs  
35 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :205:

118

GACCGCCCAN NNNCATCCAA AACTTCTAGG CACAATCTAT ACTGCTGCTG 50  
AAGAAATTGA AGCAGTTGGG GGAAAGGCCT TGCCATTGAN TTTTGATNT 99

5 (2) INFORMATION FOR SEQ ID :206:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 118 base pairs  
(B) TYPE: nucleic acid  
10 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :206:

GTACCTTGGG NNNNNNANNG GGAATGAGGT TCTACCACTC TGGAAAATTC 50  
ATGCCTGTCA NTNTAANTNC AGGTGCCAGT TNNCNNTAGG TCGCCAAAGT 100  
20 TGGGGTTAGN TGTTCNAA 118

(2) INFORMATION FOR SEQ ID :207:

25 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 170 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :207:

35 CACACTANCG ACCAACAATT AAAAGNCTNC TCACACAAGN ATCTTTTAA 50  
TAAAAATACC TCTTTCNTAA CTCCACTTTA ACTCCCTAAA ACCCATGTCTG 100  
AAGCCCCCAT CCTGGTCAAT AGTACTTGCC CAGTACTTTT AAAACTAGGC 150  
40 GCTATGCATA ATACCCTCAC 170

119

## (2) INFORMATION FOR SEQ ID :208:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :208:

TTCAATGAAA TGCTTGATA CAATGATATA ACAAAGAAAC CCTAAGACAA 50  
CGAGAACTTC AACTAAGTGC ACTCATGCAG AATCTCTGCG GGGAGAATTT 100  
TTTCTCGGGG AAGTAACCCT GCCTTTGAA 129

## (2) INFORMATION FOR SEQ ID :209:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 190 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :209:

CTTGGCGTCA TTTTCTGTAC TTCTGACAGT GCCCTCAGAG TCTGCAGGTG 50  
GATCCTTTTT TGCATGGCAT TAATTATATG AGCAGCCTCC TTCTGACAAT 100  
CCAAATTTTG GCTCCAGAGT CATTTCTGAA NNTCTACACT TANGGNCTTN 150  
AGCNTGCTCA TTCAAGGTNA AGGGGAGTTT TNAAAAATAT 190

## (2) INFORMATION FOR SEQ ID :210:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 base pairs

120

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :210:

TCATTGAGTC ATCCTTTTTG CCTGCTGCTG TAAGGTTTTT TTTCTTCTAG 50  
10 TAACTGTATG ATCCAGAGCG ACCCAGCAAG GACTCAATCG ATCACCAACT 100  
GATGCAGAAC TGTTTCATAT CTAGAAATG 129

## 15 (2) INFORMATION FOR SEQ ID :211:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 152 base pairs
- (B) TYPE: nucleic acid
- 20 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## 25 (xi) SEQUENCE DESCRIPTION: SEQ ID :211:

CTGTAAGGTT TTCTTTCTTC TAAGTAACTG TATGATCCAG AGCGACCCAG 50  
CAAGGAATCA TATCGATCAC CAGCTGATGT AGAACTGGTT TCANATCTAG 100  
30 AAATGGAANC NNNNGNGTTN TTCCTTAATG GACCCCCCN GGGGCNGAAT 150  
GG 152

## 35 (2) INFORMATION FOR SEQ ID :212:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 186 base pairs
- (B) TYPE: nucleic acid
- 40 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

121

## (xi) SEQUENCE DESCRIPTION: SEQ ID :212:

CTTAACCCCTT TGAAGGNTT GACTGTGTGA CCCGCAGCAA ATAATTCATG 50  
5 TCGAAAGATG AAAACAATA AGTTCATAAC CCCCTGCCCCG CCATTGACCT 100  
CCCTTTNAAA ANCGAGACCA AGACTCCATC ACTGGTTTCG AATTACATC 150  
10 NAACTGCTAA GATTGATACA TTNCAAGTCT GCAAAT 186

## (2) INFORMATION FOR SEQ ID :213:

## (i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 152 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID :213:

CTTAAATGCC TGTGTGATA TCTTCTTTAA ACCTGGAGAG ATTGAATCAA 50  
25 CCTTTCTCTA AAATTCCTTT CCTTTGCCTC CTCCTCTAAC TTTTCCTCCT 100  
TTCNCGCTTT TCCTCAGGCT TTGNTTTTCC TCATGCTTTG CTTCACCTCTA 150  
30 TT 152

## (2) INFORMATION FOR SEQ ID :214:

## (i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 290 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

## (xi) SEQUENCE DESCRIPTION: SEQ ID :214:

122

	TCTTCAGGAG AAGGGGCACC ACTGCTTTAA AAAACAATAC TCCNTTATAG	50
	ACTTGAACAT TTGCAGACAT TATGATCTTG CTTCCAACCTC CCACCGTATG	100
5	TCCAGCAAAC TCTCGCATGT GGCCACTAGG AGGAATGCGC AAGAATGTTC	150
	ATATTACATA TTTATAACAT TAATAACTGG AAAAAGTGAA ATGCATGTCT	200
	GTTACAGGAA AATAGGCGAA TAATCAGATA TATATATCTA NNNCCGGGAT	250
10	ATTATTCAAT AGTGGAAATG ATGACTACAG CTATACCTCA	290

(2) INFORMATION FOR SEQ ID :215:

15	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 273 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :215:

25	GTTTCTTCCA GTACATCCAA GTTTAAAATT ATTAGCGAAA TGGTCCATGT	50
	TTTTTCAATT ACTGCTGACA CGATTCTAAG CTAAGTGAAG GGGAAGATCT	100
	GAGAGCATGC TGTTTGGACT GTTGATGCAT ATTCATGATG TAACAGGTCC	150
30	TGGGCCTCAC TTTACCCCAT TCGTAAAATG GGGATAATGT CACCTGCCTC	200
	TTACCTACCT CAGAGGGATT TGCGAAGCAA ACTGTTAATC TTCGAAAACG	250
35	ACCATTACT TTAGGATAT CAA	273

(2) INFORMATION FOR SEQ ID :216:

40	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 118 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double

123

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :216:

ATCTACGGCT AGGGAGAAAC AATGTTCCCTA CATATTATGG GTAGTGAGAA 50

CATTATCTGT ATAACAGGGA ACTGTGATTA TTAAAATTA TGCAGAACTT 100

10

ATTCATCTG TGCTTTAG 118

(2) INFORMATION FOR SEQ ID :217:

15 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 197 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :217:

25 GAGGCTGGTG GCGAGGGAGT TGTGGAGGAT AACAGAAGA AAACAAGTCT 50

ATCACTAATG ACTTATTTTA CTTAGTTTCC ATTCACGAAA CCCTTTTAAA 100

TACAAGGCAA CATTTTCACA GCTGAAAAAT TACAATAA NGNNNTGATT 150

30

TACCACCAA AGCAATAGAT GTAGTTATGT ATAATCTATA GATAATA 197

(2) INFORMATION FOR SEQ ID :218:

35 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 177 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

40

124

(xi) SEQUENCE DESCRIPTION: SEQ ID :218:

CTCGCGAGCA CTCGTCCGAG AGGTCCCATATA C>NN>NN>NNNCC CAAGCCCCTC 50  
5 AAGGGCCTTT GCCAATCTNG TCATTTTATG CCAAGTCCTC TAAACGCAC 100  
TCAGGGGTAT CTACATCGCA CTTGTACAGA ATATCAAGAT CTTATCCTCC 150  
TATTTTAGGC TNCNAGGTCA AAATAAA 177

10

(2) INFORMATION FOR SEQ ID :219:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 118 base pairs  
15 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :219:

GAAATGAAAA AGAGAGCATT ATTGGAAGAA TGAAAAATAC ATCTCAGAAA 50  
25 GAAACCTANT AGTTCAACAA ATTAAAAGAA AGAAAGAAAA AAAGCAAAAG 100  
TNGGTNTCAG GGCTGGAC 118

30

(2) INFORMATION FOR SEQ ID :220:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 233 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
35 (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :220:

GAGAGCCCAG CACGTCATCC CCTGATCTGA GTCTACTGAA CACCTGTTTT 50

125

ATGGACTACA CTGTCTTTTC CTTTGAATCC CCACTTCTCC TGGAAGTGTGTA 100  
CTTGGACCAC CAGGAACATC GTAAGACACA ACCCAATACA CTCACCGCAT 150  
5 TCAGACAACT GTCCAGACAC TGCCCTGACA CCACAGGGNC CCCTTTACAN 200  
NGGTTGGNGG AAATATNNTT TAATCTCAGG CCA 233

## (2) INFORMATION FOR SEQ ID :221:

10

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 235 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 15 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :221:

20

GCACACAGAT ACCATCCCAC CTTGCTTTNT GACAGGCCAG CCACACAATA 50  
ACCCTTTCCC TACTCACTAA AGCATCCCTA GGACACCAAC AATGAGGACA 100  
25 GGCAGACTTA CCCCCGCCAT CTAGAGAGAA TGTCGTTATT ACCCATAAAA 150  
CTCGACCACC CCCATATNCA CTNTTGGGTA AAAACAAACG CTTAAACCTG 200  
TGAGCCTGCC ATTCCTTTTT ACGTGTTAAT CAATT 235

30

## (2) INFORMATION FOR SEQ ID :222:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 base pairs
- 35 (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40

## (xi) SEQUENCE DESCRIPTION: SEQ ID :222:

126

GCCAATNNNN NGGCGCGAGG GNNAGAGAGA ATGGCAAACA GGGACCCGGG 50

CCTTAGGAAT TGANTGAGGA CTTAAATTTC CCCNGAGGGA GAGNAGTGGA 100

5 G 101

(2) INFORMATION FOR SEQ ID :223:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 271 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :223:

ACGGTGACTT TCCATCCCTT GAACCAAGGC ATGTTAGCCT TGGCTCCAGC 50

20

ATGTCGTCAC CATTCCAACC AGAAATTGNC ACAAATGCTA CTGGTCGGGT 100

TGACCAATTT TCTTAATGAA GTGCTGACTT CCTTAACAAT TTNTTATATT 150

25

TNTTCGACTG TAGGGCGCTC ATGAATCCAT TTCGTTAACA CCGACAATTA 200

ATTGTTTCAC ACCCAGTGTG CAAGCCAGAA GGGCATGCTC TGGGTCTNCC 250

CATTCTTGAG ATACCAGCTT C 271

30

(2) INFORMATION FOR SEQ ID :224:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 101 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :224:

127

AGTATTATTT ACTNGGTCAT CTGGGAACCT TAATGTGATT TATTTTGACA 50  
ATTACTGTGG CACATGTTTA ATCTGCAGCT CCTGGCGACT ACTGTGCTTA 100  
5 T 101

## (2) INFORMATION FOR SEQ ID :225:

## (i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 141 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear
- 15

## (xi) SEQUENCE DESCRIPTION: SEQ ID :225:

TTCATTCCCT CCAGTGCNCG NNCATGCGAC ATATACAGGN NNTGTACCGT 50  
20 AGGCGCTANT GTGTGGTACT CTGCCACGNN ANACCNCNNC TCGTCTTGAA 100  
GACCCTGTTA ANTTTGGTGA AAATAACTTT CCANATTTCA A 141

## 25 (2) INFORMATION FOR SEQ ID :226:

## (i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 218 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## 35 (xi) SEQUENCE DESCRIPTION: SEQ ID :226:

ATTTTCTTAT ACTCCTCCCA CAGATGAGTT CACAAATACA AAAANTGGTG 50  
TACATTTATA CTCAAGNACA AATCTCCAAC AGCCAAGTAA TTATAGTTTG 100  
40 TTCTGTTATG TGCAAAGTAG ATTATTTTCAT ATTTACTTGG TATGGAAAGC 150

128

AGAGTACAGG CTCAATGGAC AATAATCATT AAACACACAT TATNTTTAAG 200

AAAANGCTGT TNNA AAAA 218

5 (2) INFORMATION FOR SEQ ID :227:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 209 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :227:

GAAAACTTTA TTTGTCCACA CCAGGATTAC CGAACAGAAN NACNNGGTGG 50

TGAGAAGTTG GTATTNATAG CACCTTATTT ACATGATGGA CTTGAGGAGG 100

20 CAGTTAATCC TATGGTTGTG TATCACAACC TTTTATTAGC AATGCCATCT 150

TCGTCTTGCC TCCNCCCTAC TTGAATATCC CTTACGGTCA ACANCCCNCG 200

25 GGGTTGGGC 209

(2) INFORMATION FOR SEQ ID :228:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 179 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :228:

TTNNAANC CAAATGGTTA TTTATTCTAA AACTGGAAGC TACTTTGCCT 50

40 ANCATTTTCG CCAGAATGGT GTAATGNNNA CAGGGGAGGA AAAAAGTTAC 100

129

AGATGTAAAC AATGACACAG TTACATTTTT TTTTAAATG GTAAAACCCC 150

TTTTTACTGG NCNTTCCAGA ANCTTACAG 179

5 (2) INFORMATION FOR SEQ ID :229:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 184 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :229:

AGTTTAATCT CANNNNNNNA TGTCAAGT TATTGTAGCA GTGAAACAAT 50

GAGGGCATACT ACTATATNGA AAAAAAACC TCCTCCCTNA TTCTCAGGCC 100

20 AACCACAGGC TTCTGCCCTG CAAAGATCAC CAATGTCAAT AGTTTGGTAA 150

TACACCATCA TAAAGGNTCC TAAATTCATC TCTA 184

25 (2) INFORMATION FOR SEQ ID :230:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 140 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :230:

GAGACAGATG TANNNAAAGT TCAGAATACA ACAGTTAAGA CTCAGTTTTC 50

TTTTTAGGTT TAGAATTGA GAGCAAGTAT TGNTATGGTG AGCTGTTTGA 100

40 GTGCAAACAT TGTGAGTAT GTTGTCAAAC GTCTAAAAAA 140

130

## (2) INFORMATION FOR SEQ ID :231:

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 178 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :231:

CGGAGACTTG TCCAGAGAGT TGTCTCTTNT NNGTTGGGGG CCGTCCCGCT 50  
15 CCTAAGGCAG GAAGATGGTG GCNNNTNNG ACGAAAAAGT CGCTGGNGNN 100  
NATNAANTNT AGGCTCNAAN TNNTTATGAA AANTGGGAAG TAANTNNTCG 150  
GGGGTAAAAG NAANATNNGA ANATGGAT 178

20

## (2) INFORMATION FOR SEQ ID :232:

## (i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 210 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :232:

GAGCCAACGC CACNNNNNAG NTGAACCACA CTCACGAAAA AAACNCNTAC 50  
35 CGTCGTCNTA ATACNNANTC TTCCCATACA AAAATCGTCC NTNTAAATNT 100  
NNTAAACCAA TTCACAGCCC ACAGAACNAA TCAGTAATTT TATANCTTCN 150  
NCGAAACCAC ACTTATCCCC ACCTTGGTCT ATTCATNACC CGGATNGAGG 200  
40 GCAACCANGG 210

131

## (2) INFORMATION FOR SEQ ID :233:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 247 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :233:

ACTGTGCGAG TAGCTTNAAA ANNNNNNNNN NNACTCAGTT TNATTTATAC 50  
AAAAAGAAAG GGGTGTGNAG TCCATGGTGT TGTACAGTNT NTAATTAGNC 100  
CANNACGAGA AAANANATNN NNNTNNNAAA NNNTGAATTA TGGGGTNAGG 150  
ACTNTCTNAC NTTCAAACNA NTATTNCACG TAAAAAACAT CACAGTGCGA 200  
AGAAAGNNAN CNCANNTAGA GCANGAAGAC ATCAAAAGCC AGCCGGG 247

## (2) INFORMATION FOR SEQ ID :234:

25

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 169 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :234:

AAACACCAAA NAAANNNNNC NAGCAANAAA GTGGAAGACT AACCAAGATT 50  
GTGGACATTG GAATGTTTAC TGTTATTCTG TGTAAGAAAA CAACTNACAA 100  
AAAAGAAAA TGGNCAACAA AATTGTTTCC CGGCNAGGCT GNAGGAAACC 150  
NGGGGGAAAN TGCCNGGGC 169

132

## (2) INFORMATION FOR SEQ ID :235:

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 51 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :235:

GCANCAANA AAGGAGACGN NANAGCAACG CAGAGATAGC CATCCAGATA 50  
15 G 51

## (2) INFORMATION FOR SEQ ID :236:

## (i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 101 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID :236:

CAAGTGTAAG TGCTTGCACC TCTCTNCCTC CCCGANTGAA CTCTCTGATC 50  
30 TCAAACCTTT TTAGGAAAGC CAGATTAAAA GCAGACGTAC CTAAATNCAA 100  
A 101

## 35 (2) INFORMATION FOR SEQ ID :237:

## (i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 156 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :237:

5 CATTATAAAA CAGCCTAACT TCCCTTATGC CATATGATTG CCTTAAAAAG 50  
ACCAGATCTC AAGGAAAAGA TCATCAAAGA GCAGAGATCT TGAAGCGGCA 100  
CAGTTTTCCA GCAGTTTTCG TATTNNTTTT TATTTACGAA TGCCATACTC 150  
10 TGTTTT 156

## (2) INFORMATION FOR SEQ ID :238:

## (i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 148 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID :238:

GCAGNCTAAT TGTGAATCTA AGAAACTACT CATAGACATC CCACCCTAAT 50  
25 GATTTTACCT NNAACNTTGT TCCTTCATCA TAGAACCCTA GCAACATCCA 100  
CCTCCTGTAG CACGAAACGA ATCAAACAAC CCCCTGGATA ACCTCTCA 148

## 30 (2) INFORMATION FOR SEQ ID :239:

## (i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 258 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## 40 (xi) SEQUENCE DESCRIPTION: SEQ ID :239:

GAGTTTTTAAC TTAATCACCT CTTTAAAAGA CCTGTCTCCA AATACAGTTA 50

134

AATTTGAGGT ATTGAGGGTT AGGACTTCAA CATGTGAGTT TGGGAAGGGA 100  
AGCACAAAAT CAGCCCCTAC CATGGTATAT TTATCATTGA TACATTACTA 150  
5 TCAACTAAGC TCAAGATTTT ATTCAGATTT GACTAGTTTT TCCACTAAGG 200  
CCCTTTTTCT TTTCTAGGNT CCCACAGAGG ATACATTACA TTTACTTACA 250  
TCTTCTCT 258

10

(2) INFORMATION FOR SEQ ID :240:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 377 base pairs  
15 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :240:

GAGCATTATT TGATGCAGAA GTTGAAAAAC AATAGACTCA AGAAAGAAAA 50  
25 CAAACCAGTG ATTCCCCTTC CTCAGATACT GGGACTAACA GCTTCACCTG 100  
GTGTTGGAGG GGCCACGGAG CAAGCCAAAG CTGAAGAACA CATTTTAAAA 150  
CTATGTGCCA ATCTTGATGC ATTTACTATT AAAACTGTTA AAGAAAACCT 200  
30 TGATCAACTG AAAAACCAAA TACAGGAGCC ATGCAAGAAG TTTGCCATTG 250  
CAGNTGCAAC CAGNGGAGNT CCTTTNAAGN GNAACTTCTN GNATAATNNC 300  
35 AAGGGTNAAC NTNTTTNNAA ANNGGCCNAA NCNNGATTTT GNACNCCCTT 350  
TNNCATTGGC ATTNANTGAA AAAAGTT 377

40

(2) INFORMATION FOR SEQ ID :241:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 114 base pairs

135

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :241:

GGNGCACTGN TCCGAGAGCT TTTTNNCTG AAGAATAGCA TCTTTAATGA 50  
10 GTGTNCTAAT CCTTGTCATC TGAAGTTTGG AAATATATTT CCCAGGGTCA 100  
GAACAATACA GAGA 114

15 (2) INFORMATION FOR SEQ ID :242:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 122 base pairs  
(B) TYPE: nucleic acid  
20 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :242:

CTCAAAATNC TGTGACAAAT TTNNNNGGTC AAGTTGTTNN CCATTAAAAA 50  
GTACCTGATT TTCAAAAACC TAATAACCTT AAAACCNCCC CACGNAAAAA 100  
30 AAAAAANCNA AAGNGGGCCC CC 122

(2) INFORMATION FOR SEQ ID :243:

35 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 171 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
40 (D) TOPOLOGY: linear

136

(xi) SEQUENCE DESCRIPTION: SEQ ID :243:

50  
GAGAATGGGA AGCCTCATTT TGGGGACAAG AACCTGTACA AGGATTTGTG  
5 ATGAACTTTT CCAATGGGGA AATTATAGAC ATCTTCAAGC CAGTGCGCAC 100  
NTATGATATG CCTCATGATA TTNTTGCATC TGAAGATGGG ACTNTGTACA 150  
TTGGNGATGC TCATCCAAAC C 171

10

(2) INFORMATION FOR SEQ ID :244:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 235 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :244:

50  
AACTTTACTG TCAGATAATA AAATTAGGGC TTTCTCTTAA AGGGCTTCTT  
25 TAAGAGAAAT ACAGAGTGTT TGGTATNTGA GAGAAAAAAA GTTAAACAG 100  
GACTTTCAAC TTAATCCAGA CTCCTAACA GTGTTTACAT GTGAGGGAAA 150  
CTCCTTTAAG TAATGCGTAG TGTTTTATTT TTACCATCAT TGGNGACAAA 200  
30 AAAAAACAAA ACATAAACAT CTNANGTGAA ATATA 235

30

(2) INFORMATION FOR SEQ ID :245:

35

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 211 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

137

## (xi) SEQUENCE DESCRIPTION: SEQ ID :245:

GGCCTAGCCT GCCATACCCT TACGAGCAGG CTCAGTGATT AGACTTTGAG 50  
5 TCTAAGTTAA AAACGCCCTG CCCCTTCTC GCAGGCCACC TACACCGTNN 100  
TTTTATCGAT TTGATAAAAC CACCAGCCTA CTCATCAAGN NGCACCCCTGC 150  
NTNTACNTCT AACNTAACA TNACNGCGGC CACCTACTCA TGCCCTANTG 200  
10 CAGCNCACCC T 211

## (2) INFORMATION FOR SEQ ID :246:

15 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 194 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear  
20

## (xi) SEQUENCE DESCRIPTION: SEQ ID :246:

25 GGCTGAGAAT CCTTGAGCTT ACCATTTGAT ATTTCTATAT TATTTAAGAA 50  
AAGTCAAAAG ATTTTGAAAA CAGCAATAGA AGTAAGATCC TTTAAGCTCT 100  
ATTTGCAGCC CCTAAGAAAA GTGATGAGGA CACTGTGCAT GCCCATATGT 150  
30 GAACATGGTG GTACCTTAGG NATTTCCCTT TNTCNATGAA TATA 194

## (2) INFORMATION FOR SEQ ID :247:

35 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 249 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear  
40

138

(xi) SEQUENCE DESCRIPTION: SEQ ID :247:

	GCCCCCTCAA GGGCATCCTG GGCTACACTG AGCACCAGGT GGTCTCCTCT	50
5	GACTTCAACA GCGACACCCA CTCCTCCACC TGACGCTGGG GCTGGCATTG	100
	CCCTCAACGA CCACTTTGTC AAGCTCATTT CCTGGTATGA CAACGAATTT	150
	GCTACAGCAA CAGGGTGTGG ACCTCATGGC CCACATGGCC TCCAAGGTAA	200
10	GCCCCCTGGAC CACCAGCCCC AGCAAGGCAC AAGAGGAAGG AGAGACCCT	249

(2) INFORMATION FOR SEQ ID :248:

15	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 248 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :248:

25	GCCCCCTCAA GGGCATCCTG GGCTACACTG AGCACCAGGT GGTCTCCTCT	50
	GACTTCAACA GCGACACCCA CTCCTCCACC TGACGCTGGG GCTGGCATTG	100
	CCCTCAACGA CCACTTTGTC AAGCTCATTT CCTGGTATGA CAACGAATTT	150
30	GCTACAGCAA CAGGGTGTGG ACCTCATGGC CCACATGGCC TCCAAGGTAA	200
	GCCCCCTGGAC CACCAGCCCC AGCAAGGCAC AAGAGGAAGG AGAGACCC	248

35 (2) INFORMATION FOR SEQ ID :249:

	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 82 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
40	(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :249:

5 GGAGGGGACC GCAGCATCCA GCCCTCTAAG GCCGGGCAGC GGTCCGCTTG 50  
GGGCAGAGCG CAGCGCAAGC AGGCTCAGTG TA 82

## (2) INFORMATION FOR SEQ ID :250:

10 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 125 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear  
15

## (xi) SEQUENCE DESCRIPTION: SEQ ID :250:

20 GGGGCCCTCA GGACATCCAC GTGAGCGTCT GCCCAGCTGC ACTGATATTG 50  
TNTTGCAAAT CCAGATTTGT TGNCATTACT GATGGGCGCG TGAAACCAGN 100  
GAGAGATGCA CAAGATTTAC AGGCC 125

## (2) INFORMATION FOR SEQ ID :251:

30 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 130 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :251:

35 GGCCCAGAGG TCCTTTACTC TTACGGNACA CCTTAGCCAC ATTCACAGGG 50  
40 AATGNTCCAG CACTCAGGCT CCTTCCCATN GGTTTTCAAA AGCGCGTTTT 100  
TCTGGGGGAG CGGCCGCCTT TAGTCGACCC 130

140

## (2) INFORMATION FOR SEQ ID :252:

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 216 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :252:

GAGAAGGCTG GAGAAAAACC ATCCACACAT AAACAATNGN ATTTACTCNA 50  
15 AAATNAAGTA CAGGTTTCAG GTATTTAAAA TAAATAAAGA AAAATCTCGT 100  
TTCCTTTGGC ATCTTTAGAA AATAAACTAA GCAATAAAAG AGGTGATTGT 150  
ATAAAGACAT GCGTAAGCAA ACATATGGGG AAAACCAGCA ACTTGGTTTT 200  
20 ATGNGATAAT ATCAGC 216

## (2) INFORMATION FOR SEQ ID :253:

25

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 249 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :253:

35 GGAGAAGGAG GCTGATTGCG TACATCCAGC AGTTACAATT TTTAAAAATT 50  
ACANTNNNNC NNTTNGATTN TTAATNTANG TAATTTCCTT CCAAAGAAGN 100  
TTCACATGTA ATAAGTAGAA ATTCTGTATA GGAAAAAAGC ATTAAAAATA 150  
40 TANATACNGC TTCATNCGTT GGGAACCATT AAAAGTAATA TAATNAGCTT 200

141

TTTTCAGAAG GATCTTTTGT AGCAGTGNTT ATGAATGNAC CCGCAAAAT

249

(2) INFORMATION FOR SEQ ID :254:

5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 166 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :254:

15

GACCCCATTC TATATTATNC GTNNNGCGAT TTTTtagcca CCCTGAAGTT

50

ATATTTNTAT ACCNAGGCTT CGAATAATCT CATcNGACTN ACCACCCTNG

100

GAAAAAAGA ACCGTTTGAT ACATAGGNAT GNTNAGCTTG ATATCAATNG

150

20

CTCCCTGGGN TTCTTG

166

(2) INFORMATION FOR SEQ ID :255:

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 223 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :255:

35

CCAGACCAAC CGCCTGCAGG AGGCTCTGAA CCCTCTTCAA GAGCATCTGG

50

AACAACAGAT GGCTGCGCAC CATCTCTGTG ATCCTGTTCC TCAACAAGCA

100

AGATTTGCTC GCTGAGAAAG TCCTTGTTGG AAATCGAAGT TGAGGACTAC

150

40

TTTCAGAATT TGCTCGCTAC ACTACTTTGA GGATGCTACT CCCGAGCCCC

200

142

CTTCTNTTGT NACAGACAGC AGA

223

## (2) INFORMATION FOR SEQ ID :256:

5

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 292 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :256:

15

GGAGAAGAAG GAGCAGGAGG TGATGCTACT GACTCAAGTC AAACAGCTCT 50

TGATAATAAA GCTTCATTGC TCCATTCAAT GCCTACTCAC TCCTCTCCGC 100

TCTCGAGACT ATAATCCATA TAACTATTAA GATAGCATCA GTCCCTTCAA 150

20

CAAGTCTGCC CTCAAGGAAG CCATGTTTGA TGATGATGCT GACCAGTTTC 200

CTGACGATCT TTCCCTAGAT CATTCTGACC TGTGTAGAG TTGTTGAAGG 250

25

AGCTGTCTGA CCATAATGAG CTGTAGAAGA AAGAAAAATT GC 292

## (2) INFORMATION FOR SEQ ID :257:

30

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 238 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

## (xi) SEQUENCE DESCRIPTION: SEQ ID :257:

AAGGAGCAGG AGGTGATGCT ACTGACTCAA GTCAAACAGC TCTTGATAAT 50

40

AAAGCTTCAT TGCTCCATTC AATGCCTACT CACTCCTCTC CGCTCTCGAG 100

143

ACTATAATCC ATATAACTAT TAAGATAGCA TCAGTCCCTT CAACAAGTCT 150  
GCCCTCAAGG AAGCCATGTT TGATGATGAT GCTGACCAGT TTCCTGACGA 200  
5 TCTTTCCCTA GATCATTCTG ACCTGTTGTA GAGTTGTT 238

## (2) INFORMATION FOR SEQ ID :258:

(i) SEQUENCE CHARACTERISTICS:  
10 (A) LENGTH: 137 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

## (xi) SEQUENCE DESCRIPTION: SEQ ID :258:

GGAGAGAAAA GTTCCTGAGT GACAGAGAAA AAGAACAAAA AGCTGCAGAA 50  
20 GGCNTCAGCA GAGGCCACTG CTGGCCCTGA GGCTGCACCA AGTGACGAAG 100  
AACCGGCTCC AAGCATTCGT CACAGCACTA ATTTAAA 137

## 25 (2) INFORMATION FOR SEQ ID :259:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 241 base pairs  
(B) TYPE: nucleic acid  
30 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## 35 (xi) SEQUENCE DESCRIPTION: SEQ ID :259:

GCGCGACTTT TAAGGGATTT GCNGTGATGC CTGTTGACCC AGTGCCTTCC 50  
TAGCCGGGAA GGGGCTCGGC TGGAGTGNN AAGCTCAGAA AAATTTGCGC 100  
40 AAGAAAAAAA CCTATGAGGT AATAATAGGA TTATTCCGTA TCGAAGGCCT 150

144

TTTTGGACAG GTGGGTGCGG TGACCTTGGT ATGTATTTTT CGTGTTACAT 200

CGCGCCATCA TTGGATATGT TAGTGTGTNG GTTAGTAGGT C 241

5 (2) INFORMATION FOR SEQ ID :260:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 248 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :260:

GCGGACTTTT AAGGGATTG CNGTGATGCC TGTGACCCA GTGCCTTCCT 50

20 AGCCGGGGAA GGGGCTCGGC TGGAGTGNA AAGGCTCAGA AAAATTTGCG 100

AAGAAAAAA CCTATGAGGT AATAATAGGA TTATTCCGTA TCGAAGGCCT 150

TTTTGGACAG GTGGGGCGGT GACCTTGTA TGTATTTTTC GTGTTACATC 200

25 GCGCCATATT GGTATATGTT AGTGTGTTGG TTAGTAGGTC TCGTATGA 248

(2) INFORMATION FOR SEQ ID :261:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 239 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :261:

GGATCTTTCA GGTGATGAAA TAGTTCTGTA TCTTGATTTT GGCGAATCTA 50

40

CACANGTGAT GAAGTAACGT GATAAAATGA CATAGACCTG TATGCCTACT 100

145

ACAATACAGT ATCAAAACCA GGGATTGATT CCTGGTTCTT TTCCAAATCC 150  
ACTTCCCAAA CTTATGGTAA GGTAATATTA AAAAGGCACC AAAGAGCCCT 200  
5 GATCCCTGGA TAAACAGGAT CATTTCAAAG NNGTTTATA 239

## (2) INFORMATION FOR SEQ ID :262:

(i) SEQUENCE CHARACTERISTICS:  
10 (A) LENGTH: 143 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

## (xi) SEQUENCE DESCRIPTION: SEQ ID :262:

GCCGGGTGAT GGCCAGGAAG GTGCCCTCTG TTTTGTGTA AACAGCCATT 50  
20 GGCCTTTGTC ATTGAGTCAC CACCTGCAGG GCTTGGGAGT GAGCGTTGGG 100  
TAGGNTCAGG CCCCCAGAAC CGCCTGGGTA CTCACCGCTA GCA 143

## 25 (2) INFORMATION FOR SEQ ID :263:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 246 base pairs  
(B) TYPE: nucleic acid  
30 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## 35 (xi) SEQUENCE DESCRIPTION: SEQ ID :263:

GGCGCTCAGC CTCCCCAAGG ACAAGCTCCT CCCCCTGTAA TACCTCCTCC 50  
TAACAGCCGG ATATGGATGG CAAGTTACCA AACACAGTGA GCCGGGACTC 100  
40 TAAAAAATA TAGCAATCCA GATAGGCTTC GATTTCCTGT GACACTCTGA 150

146

AGACATGAAA GTAGACATCG AAAATGAAAA TANTTATNNA AATGAAATGT 200  
TTGGAACCTT TAGCACAGAT TTGTTTGGGA AGACACGGTC TTTTAG 246

5 (2) INFORMATION FOR SEQ ID :264:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 199 base pairs  
(B) TYPE: nucleic acid  
10 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :264:

GGCTCCATTA AGGACCAAAT TNATGCTACC ACTAAACAAA AANNTATAGT 50  
CTGTGTTAAA TCGTATGCTT TTAAAGGTA TTAAAGATT CAACTAGCTT 100  
20 TAAAGAGGCT GAGCAGCTCA GGAAGCCTGT AATGTGACAT AACTCTTTGG 150  
ACCTGATCTT GATGTTCTGC TGTTGTNAGT CTTGAAGAGC GTATNTGAT 199

25 (2) INFORMATION FOR SEQ ID :265:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 245 base pairs  
(B) TYPE: nucleic acid  
30 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :265:

GGTTTCAATC GTCCATCCAA GATACAAGAG AACGCATTGC CACTGATGCT 50  
TGCTGAGCCC CCACAGAACT TAATCGCCCA ATCTCAGTCT GGTACTGGTA 100  
40 AAACAGCTGC CTCGTGCTG GCCATGCTTA GCCAAGTAGA ACCTGCAAAC 150

147

AATATCCCGT GTCTTCTCTN TCCCAACGTA TGAGCTGCCC TCCAAACAGG 200

AAAAGTGATT GAACAAATGG CAAATNTTAC CCTGAACTGA AGCTG 245

5 (2) INFORMATION FOR SEQ ID :266:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 121 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :266:

AGGAAAAGAT GGAATATGT TTCTTTCCTT TGAGAATTCA CAAAANGGGG 50

TCAAAAACAA AGCAATGCTG AAAGCGAACA TCCATTNGC CTGCAATTCA 100

20 AGGCGAAAAT CCAAAGGCAT C 121

(2) INFORMATION FOR SEQ ID :267:

25 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 169 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :267:

35 GGGTCGCTCT CCCCCCTCT TTCTTCGGGT TGTGTGCGTC TCCGCTTTCG 50

TGATGTGAGG AACTCTGGGG TGGGCGACGG GTCCAACTCG CGTTGTCATC 100

TCCCAGGTTG GTACACCCCC CCCCCGTTTC CCCAGCCACA CTCCACGGCC 150

40 AGGGTGGAGG CAGATGTCT 169

148

## (2) INFORMATION FOR SEQ ID :268:

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 200 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :268:

TCGCAGGAGA GGAATTACAT GCTCATCCTA GAAGGGGGGG CTGACTGCAG 50  
15 GTGTTGCTGG GAAGCCTCTC CAGGCCTGGA GCTGGAGTAC CCGTCCTCAG 100  
CACTGCCAGC AGAAAAAGTT GTGATTCAAG GAAAGCACAT TGAATGCATT 150  
ATAGCAATCC CAGACCTAAG TTCGAAGTTG CTTTGTAAAC AGTGCTGCCT 200

20

## (2) INFORMATION FOR SEQ ID :269:

## (i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 163 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :269:

AGGGGGGGCGC AAGAGAGAAG AACTTCACAC TTCTTTATTG CTCAGCCTAG 50  
35 ATAGCAGCAG CTGGGAATAC GTAGGACAAA CAGGACGTCG AACAAATTAC 100  
TCCACTATAT TAATATTCAC TACACCACTT ATTCTTTCTT GAATTGTAAA 150  
CACTAAGTGT AGT 163

40

## (2) INFORMATION FOR SEQ ID :270:

149

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :270:

10

TCACACTTCT TATTGCTCAG CCTAGATAGC AGCAGCTGGG GAATACGTAG 50  
GACAAACAGG ACGTCGAACA AATTACTCCA CTATATTAA TTCACTCACA 100  
CCACTTATTC TTTCT 115

15

## (2) INFORMATION FOR SEQ ID :271:

## (i) SEQUENCE CHARACTERISTICS:

20

- (A) LENGTH: 178 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID :271:

30

CCCGAGACCT GCGANAATGG TGCTGTGACG ACGAATAGCC ACGCATTATA 50  
GGGTNTTNTG TTATGGGGGA CACTCTACTA CGGGATGCGT ATGATGNNGN 100  
NCCATTATNG NAGTGGGCAT TGGGGGGAAA CAGAGCACCT GATGCTTTAC 150  
TGCAGAAATN CCTATGTGAC TCTTATAA 178

35

## (2) INFORMATION FOR SEQ ID :272:

## (i) SEQUENCE CHARACTERISTICS:

40

- (A) LENGTH: 178 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double

150

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :272:

CCCGAGACCT GCGANAATGG TGCTGTGACG ACGAATAGCC ACGCATTATA 50

GGGTNTTNTG TTATGGGGGA CACTCTACTA CGGGATGCGT ATGATGNNGN 100

10

NCCATTATNG NAGTGGGCAT TGGGGGGAAA CAGAGCACCT GATGCTTTAC 150

TGCAGAAATN CCTATGTGAC TCTTATAA 178

15 (2) INFORMATION FOR SEQ ID :273:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 135 base pairs

(B) TYPE: nucleic acid

20 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :273:

CTCTAGTAAA AATGTTTGAG GAAACAAAAA TGGGGAAGAA GATCAGAACA 50

AAAANATTGT TAACACTGAC CGTCCTCATG CAGGTAGGCT ACTACCAACG 100

30

CTGGTTGTTA CTCCAGGAAA ATCGAGGTGA ACATC 135

(2) INFORMATION FOR SEQ ID :274:

35 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 231 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

40 (D) TOPOLOGY: linear

151

## (xi) SEQUENCE DESCRIPTION: SEQ ID :274:

TGTTCGAGGAG AAGAAACCAC TTGATAACAC CCCGCGACAT CGTGGGGCTG 50  
 5 CTTGTCACAN GAAAGCACCA TGTTGCAAT GGATTGCTGC AGGTGCTGCC 100  
 GTTGCCCTCCT CAGGGTCTGC TGAAAGTCAT CTTCTAGGGT CTGAACGACA 150  
 TAACGCAGGA AAAGGACTCG CCCAGGCAGA GTTTGTCCCT CTCCTTCAT 200  
 10 GACATAGGTG AGCAGTTTCC AGTCCCACTC C 231

## (2) INFORMATION FOR SEQ ID :275:

15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 170 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID :275:

25 TCGCAGGAGA AGAAACCTNG TTGCTCCACA ATGCAACCAC ACTGATTTTC 50  
 TCTTTTCTCT NNAGTTNTCC TTGTCTGTAA CAGGAATGTC CCTTACTATA 100  
 GCAGGCGGAC ACGGCCATGG GTCAAGCACC CTGCTTCTGG AACTTGNNNG 150  
 30 NCGTNCCCAC CATTGATTGA 170

## (2) INFORMATION FOR SEQ ID :276:

35 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 315 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

40

152

## (xi) SEQUENCE DESCRIPTION: SEQ ID :276:

	ATATGAAGGA GGAAATGGCT CTCACCTTCG TGAATACCAA GACCTGCTCA	50
5	ATGTTAAGAT GGCCCTTGAC ATGAGATTGC CACCTACAGG AAGCTGCTGG	100
	AAGGCGAGGA GAGCAGGATT TCTCTGCCTC TTCCAAACTT TTNTCTGAAC	150
	CTGAGGGAAA CTAATCTGGA TTCACTCCCT CTGGTTGATA CCCACTCAAA	200
10	AAGGACACTT CTGATTAAGA CGGTTGAAAC TAGAGATGGA CAGGTTATCA	250
	ACGAAACTTC TCAGCATTAC GATGACCTTG AATGAAAATN GTACACACTT	300
15	AGCGTAGCAT ATTNA	315

## (2) INFORMATION FOR SEQ ID :277:

## (i) SEQUENCE CHARACTERISTICS:

20	(A) LENGTH: 209 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID :277:

	ACGTTCTGCG CCTTCCTAGG AGAGTCTTAC AGTGTTGAGA TTTCACAAGC	50
30	AATGCGAGTG TAAAATACCA GCTCTACAAG AAGCTAGGCT CTGTGACGGC	100
	ATAGTTTCA GTAGCTTTAT CACAATGAAA CGAGAATTAT ATGACATGGT	150
35	AGCAGAAATA GGCCCTTTTCG TGNGCTGTTT TATTTNCTCG GATNGTAGAT	200
	ATAGTAATC	209

## (2) INFORMATION FOR SEQ ID :278:

40

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 107 base pairs

153

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :278:

10 AAGACATCCT AAGCTATGTT GAGGAGGGAG AAGATCTGAG ACTCAAGTTC 50  
TGCTGTTAAC CATGAGGTGA TTTAGTAGCT AAGTACGCCT TAGCCTTTTA 100  
GAGTCTT 107

15 (2) INFORMATION FOR SEQ ID :279:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 276 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :279:

ATGAAGAGAA AACCATCCTC CCATATGAAA ATATTTGCAG TAGGAGAACA 50  
CAGTGCAATA GGCTCCAAA ATGGCTTTTA AGACCTTTGG NGGGGCAGTT 100  
30 ACTACTGCTT TAAAAGCCAG GTTAAAGTAT ACTCTAAGCA AAGATGACCG 150  
TAGAGCAGCT AGCTTCCTTT TCTATAANNA TAGGGAAAGC TCTCTCCATC 200  
35 GTCCATCAAA TCAGCTCTAG AAGGTTTTTC TTTCCCNCT ATAAGTGCAC 250  
AAAGGGGAAA CACTGATTTT AAGCTT 276

(2) INFORMATION FOR SEQ ID :280:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 185 base pairs

154

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :280:

AGGAACAGGA TAGGTGTATG CATACTACGG CTAAGGAGAA ACAAGTCCTA	50
CATACCAGGG TAGTGAGAAC ATTACCGCAT AACAGGGAAC TGTGATTATT	100
TAAAAACGC AGAACTTATT TTATCCGTGC TTAGAAATA ACTGTATACA	150
GTGTTATAAG TTGAAAAGAA CTCAAAACAA CCAAT	185

(2) INFORMATION FOR SEQ ID :281:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 186 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :281:

AGGAACAGGA TAGGTGTATG CATACTACGG CTAAGGAGAA ACAAGTCCTA	50
CATACCAGGG TAGTGAGAAC ATTACCGCAT AACAGGGAAC TGTGATTATT	100
TAAAAACGC AGAACTTATT TTATCCGTGC TTAGAAATA ACTGTATACA	150
GTGTTATAAG TTGAAAAGAA CTCAAAACAA CCAATA	186

(2) INFORMATION FOR SEQ ID :282:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 198 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

155

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :282:

TGTGGGCTCA GTAATGTCCC CGCTGATGAC AATTTGAGA GTCCATGTTT 50

TATAGAAACC TTGAGGTCGG CCAGCCGTGT CTTGGCCAAT GAGATGTAGT 100

10

TGTGAGGAGG GGGCGTACTT GGGGACCAGG GGTGGGTGGA GATGTGCCCT 150

GTAGGCACAG GGAGACTCAA AAGCACGAGT TNTGAAAGCG TAAATGGG 198

15 (2) INFORMATION FOR SEQ ID :283:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 222 base pairs

(B) TYPE: nucleic acid

20 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :283:

AGAAAAAGGT GAAGCGAAGC CCAAGGACAC CATGCTAAGG GCAAAAGTAA 50

GAGACAGTCT CAGAACTGAG AGAATCGTGT CTTCTGCTTT TTGAAGTAGA 100

30

CTGTCACACT CAGGCAGCCT GTCAATGCTG AATGTTAGGA CTTCTGTCTC 150

CGCTGGAGAC ACGCCTGGGC AAGTCAGCGT TTAGTGTTG ACAGCTTTCT 200

35 CAGCTCCCTG ACTCCGTTTA CC 222

(2) INFORMATION FOR SEQ ID :284:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 162 base pairs

(B) TYPE: nucleic acid

40

(C) STRANDEDNESS: double

156

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :284:

ATGGATCAAA CTACCTCTAT AATGAAGACT GTTCTCAAAA ACGCGAGGNA 50

10 ATGTGNGACG ACACTGACCT ATCAGACAAG AGGGCATGCC CCCCTGGCCA 100

CCTTTGNCGC TGTTTNTGCA ACGTTCGCAG TGNTACTCTG CGTGAACCGG 150

TAGACTGCTT GG 162

15 (2) INFORMATION FOR SEQ ID :285:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 67 base pairs

(B) TYPE: nucleic acid

20 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :285:

GGATCCANGC AAAGCCCACT CCTCCAGGGT GAAGTTTTTC TCCCGCGACA 50

30 GACAGCAGAC TCGAGCC 67

(2) INFORMATION FOR SEQ ID :286:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 153 base pairs

35 (B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :286:

157

GGTCGGATCA GGTCAACCCGG CAGCAGCAGC TCTCGAGAGC TGAGGCACAA 50  
GGCAGGGGGCC CGGCTGTACA CCTGCAGGAC CCAGGAGAGC CTGTTGCAGT 100  
5 TCTTGTCCGA AGCGCCGAGA TAGCCACTCA GTGTCCCTGC AGCAGGAGCA 150  
GAA 153

## (2) INFORMATION FOR SEQ ID :287:

10

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 293 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
15 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :287:

20

TACTACGGCT AAGGAGAAAC AATGTTTCCTA CATATCACGG GTAGTGAGAA 50  
CATATCTGCA TAACAGGGAA CTGTGATATT TAAAAACAGC AGAACTTATT 100  
25 CCATCGTGCT TTAGAAATAA CTGTATACAG TGTTATAAGT TGAAAAGAAC 150  
TCAAAATAAC TGATATAAAT ACATCTATGT ATTAGAATTT AAAAAAGCTG 200  
CTTTCTGTGA AGTCAATCAG CTATATTAAA AATGACACAA ATCCAAAACC 250  
30 GATGCATGCC ATATANAAGG GACATTGNAA GTCCGCTCGC TGC 293

## (2) INFORMATION FOR SEQ ID :288:

35

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
40 (D) TOPOLOGY: linear

158

(xi) SEQUENCE DESCRIPTION: SEQ ID :288:

AGGGTAAATG TACGTTGTTG AGTCACAGGC CTGCCAGACC TCTACTACCT 50  
5 CATTGTCCCC TCCGGTGACC AGTTCTGCCG TCACTGTCAG GAGAATGCCC 100  
GTGTTGAATC ACTG 114

(2) INFORMATION FOR SEQ ID :289:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 290 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :289:

20

ATGAACCAGT GCCCGAGGTA CCCGGGTGTG GACCAGAGAA GTTTGCTGGA 50  
AAGGACGTTG CCAGGACTTA CACGTTTACA GATCCAGCAA CTGCTCTNCC 100  
25 CAGTGCCACA ACCATGGGGC GCCAACCACA AGCAGGAGTG CCACTGCCAC 150  
GCGGGCTGGG TCCCACCCNA CTGCGCGAAG CTGCTGACTG AGGNGCACGC 200  
AGCGTCCGGG AGCCTCCCTG TCCTTGTGTG GGGTATGGNG CTCTGGCGTT 250  
30 GNGCTGGTTA CCCTGTAGGA GTTANTGNCT ACCGGAAGCT 290

(2) INFORMATION FOR SEQ ID :290:

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 179 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 40 (D) TOPOLOGY: linear

159

(xi) SEQUENCE DESCRIPTION: SEQ ID :290:

5 AACCGCTCTC CACACCGCTC CCACGAGCTC CAAGCTTAAA CGTCCAGATN 50  
NACTTTGTTG CTTTGCTGAT TTAAACAGCT TGATTCTAAG CNCTTACTAG 100  
TATCATNTGT GGCAGGACTT GNTCCATATC AGTGTTACTT TTGCTACTGT 150  
TTTGTAGAAC GATGTACATG AATGAGCCT 179

(2) INFORMATION FOR SEQ ID :291:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 199 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :291:

20 TCTTTCATTT TGNCTGCCAA TCATTGTCAG AAATTTAGGG AAGTCAATTG 50  
25 TGCCATTACC ATCGGCATCT ACTTATTAAT TATGTCCTGT AACTCTGCTT 100  
CTGTGGGATT CTGCCCAAGA GATCTCATTA CAGTTCCCAA TTCTTTGTTG 150  
TTATAGTACC ATCACCATTT CGTTAAATAG TGAAAGAGCT TTTTGAATC 199

(2) INFORMATION FOR SEQ ID :292:

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 177 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :292:

160

GGAAGACCAT TCTGATCATC CTCACTGACG CCAACGCAA GAGGGTGGTT 50  
TTCCTGAAGC AGCTGGCTGT GGCTTATACT CGTGAAGTGA CCTCTGGNCT 100  
5 CAATTGAGTT CCTCAACGAA GACCACACCA GAAATTGTCA TTGCCACCTC 150  
AACCGAANNG ATATTACAAT GTAAAAA 177

## (2) INFORMATION FOR SEQ ID :293:

10

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 295 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 15 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :293:

20

ATTGGTTTTTC CTCATCCACT GAGAATGCTG CTGGTTACTG CAAACGTTCA 50  
CCAACCANAG CTTTGGTCCA TACAGCTTTC TTCTAGATTN GGAGACTCTC 100  
25 AAGGACAGCA GGNGCTTTAA AATCCCTGGA CTGTGTTGAG AGGGCTTCTT 150  
TAGGCTTTTC ATGATGTGAA TAGCCAGTCA TGAACCTTGN GTCTGTTTCT 200  
TTTAGGCTCT TTTTGCAGCA GCAGAGCCAT GCTATNGAAG GAGTGAGAAC 250  
30 CTATGCGAGN GACCCNGTGN TTGNACTTGC CAGGGAGCTT GGCCT 295

## (2) INFORMATION FOR SEQ ID :294:

35

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 40 (D) TOPOLOGY: linear

161

(xi) SEQUENCE DESCRIPTION: SEQ ID :294:

AATGATCCTT TTTTCGCTCT TACCTATAGT ACAAGTCCAT GATACTACTG 50

5 CATATTTTAC CATTTTGNA AACTGTGAG 78

(2) INFORMATION FOR SEQ ID :295:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 163 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :295:

ATTCTGTACC TGTTCTGAAC CTCGCCATAA GGGACTTGCA GCTTCGATTT 50

20 GCTAACCTGA AATTCTGCTG CTGCCATGGA ACAAGCCTGG GCTAGCTTGG 100

GGGAGGAGGA GAGACCATGT GGAGTAGAGC CAAGCTCTGG ACATTTGAGA 150

25 GAGCCCGGTA ATA 163

(2) INFORMATION FOR SEQ ID :296:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 189 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :296:

AGCTTAGAGC GGAACGGGTT CCACGTGCGG TACTCCTGCT TCACGCCGCC 50

40 CTCGGTCACC GTGACGCGCC TCTCGCCGTA CACAGACTGG CCCGGCACCA 100

162

TGTTAGCGTG ACCAGCGCGT CCTCCGCCCC GCGTNAGATG AAGAGGCCCT 150

CGTGCCGGTG CGCTCCACCG ACACCACCAT GGCCCCTTC 189

5 (2) INFORMATION FOR SEQ ID :297:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 199 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :297:

GGAAACCAGC CCCTCACATC CTCCCTGAAC TTCCTGTCCC CACTCACACA 50

20 AGTGGTCCGG TGTACCCCTG CAGTTGGGTA TAGTCATAGG TACCATTGAT 100

GACGCCTTCT ACCTCGGCCA TGTAGGCCTT CCAGTCAACC TCTGTGTCTG 150

GAAGAAGACA AGATGATCTG GTTACTTTTG AGTCTAGAAC TTGTCTGCC 199

25 (2) INFORMATION FOR SEQ ID :298:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 181 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :298:

AAAAGATGAT AAATCCACCC TCNTGCTCTT AAAATCCCAT AAACGNTAGG 50

40 CTCTGGAGAA ACAAGTTGTT CTGTCGAGCC CTTGCCATCA ACACACTAAG 100

CAATCATAGT CCCCCAGAGC ACNAGATACT GCTAATGACC ATTANATNTT 150

163

GTATCATCAT GCTGCCTCCT GCATTGAAT T

181

## (2) INFORMATION FOR SEQ ID :299:

5

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 314 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :299:

15

AACATTGTTT ATTCATCCAG CAGTGTGCT CAGCTCCTAC CTCTGTGCCA

50

GGGCAGCATT TTCATATCCA AGATCAATTC CCTTTTTCAGC ACAGCCTGGG

100

GAGGGGGTCA TTGTTCTCCT CGTCCATCAG GGATCTCAGA GGCTCAGAGA

150

20

CTGCAAGCTG CTTGCCCCAAG TCACACAGCT AGTGAAGACC AGAGCAGTTT

200

CATCTGGTTG TGACTCTAGC TCAGTGCTCT TCCACTACTT ATATNCGCCT

250

25

TGGTGCCACC AAAAGTGCTC CCCAAAAGGA AGGAGAATGG GATTTTTTCC

300

GAGGCATGTA CATT

314

## (2) INFORMATION FOR SEQ ID :300:

30

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 168 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

35

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :300:

40

AAGAGTCCTG AAGGCATATC CAAGCCTGTT GTTCCTGCAG ACCTCATTAC

50

164

CACGCCAACA GAGAAGGCTG GACTGCTGCC CACATGCTGC TTCCAAAGGT 100  
TTTAAGAAGT GCCTAGAAAT CTCGTGTAGG CACGAAGGGC TTGAGCCAGA 150  
5 AAGGAGAGAC AAGTGCAA 168

## (2) INFORMATION FOR SEQ ID :301:

## (i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 142 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

## (xi) SEQUENCE DESCRIPTION: SEQ ID :301:

ACCCACATG CCCAGATGTC CACGNGCTTG CNATACGCCT CTTTGCAAAG 50  
20 GACCTCAGGG GACAGGTACC TGGTGTGCCA GCGAAACCAA ACCATGCCTG 100  
CTGGTTCCCC TGACCTCGAT AGCTAGGCCA AGTTTGCCAG CT 142

## 25 (2) INFORMATION FOR SEQ ID :302:

## (i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 197 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

## (xi) SEQUENCE DESCRIPTION: SEQ ID :302:

AGAATTCGTA ACTCATCCTA GAGTGGGCAC ATTTTAGACA TAGCAGGCGT 50  
GATGACCAAC AAAGACTGAA GTTCCCTATC TACGGAAAGG CATGACTGGG 100  
40 AGGCCCCACAA GGACTCTCAT TGAGTTCTTA CTCGTTTCA GTCAAGACAA 150

165

TGCTTAGTTC AGATACTCAA AAATGTCTTC ACTCTGTCTT AAATTGG

197

## (2) INFORMATION FOR SEQ ID :303:

- 5 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 236 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :303:

15 AGAATTGCAA CTCATCCTAA GTGGGCACAT TTAGACATAG CAGGCATGAT 50

GACCAACAAA GATGAAGTTC CCTATCTACG AAAAGGCATG ACTGGGAGGC 100

CCACAAGACT TTCATCGAGT TCTTACTTCT TTCAATCAAG ACAATGCTTA 150

20 TTCAGATACT CAAAAACGTT TCACTCTGTC TTAAATGAAC AATTGAATTT 200

AAAAGTTTTT GAATAAATGA TGAAAATTTT TTAAC 236

## 25 (2) INFORMATION FOR SEQ ID :304:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 220 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

30

## 35 (xi) SEQUENCE DESCRIPTION: SEQ ID :304:

ATGTCATTCT CCTCATCCTC CGCATCTCCA CTGTCGTGCA CAAGGACCAC 50

CATGTTTCCT TTAGTTCCCA GCACACGGGG CTCTGCAGTA GTGAATGAAG 100

40 TCTAGCACAG CCACCGCCCC CATGCCCAGG CTCAGGAGCA CACTGAGGTC 150

166

GTCCACCAAC ACACCGGGTA CGTCCACCGA GCCTCTCCAC TGCTCTGGCT 200  
TTAGGCCTCC CGTACAAACT 220

5 (2) INFORMATION FOR SEQ ID :305:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 145 base pairs  
(B) TYPE: nucleic acid  
10 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :305:

AGAAGAAAGG ACACCATTAC CATCCATATT GACATCGCAT TTCCATAGAA 50  
ATGCCAAAGA AAGAAGGTCC TGGGGTTTTT TATAGAAGCT CAAAAAGNTC 100  
20 AACCTTCGAT GCTATCCCCC AGCCCAATAC AAAATCAGAA AAAGC 145

(2) INFORMATION FOR SEQ ID :306:

25 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 120 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :306:

35 AGTCAAGGCA TTATGGTTTT TAATCTGAAA CTTAGAGAAC CCTTTAATAT 50  
TNGCTTTTAC TGGCGTACAT ATGAGTGGAA TATAAACTGT ACACACNNNG 100  
NGNTGATATA AACAGATNNA 120

40

(2) INFORMATION FOR SEQ ID :307:

167

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :307:

10

AGTCAAGGCA TTATGGTTTT TAATCTGAAA CTTAGAGAAC CCTTTAATAT 50  
TNGCTTTTAC TGGCGTACAT ATGAGTGGAA TATAAACTGT ACACACNNNG 100  
NGNTGATATA AACAGATNNA 120

15

## (2) INFORMATION FOR SEQ ID :308:

## (i) SEQUENCE CHARACTERISTICS:

20

- (A) LENGTH: 247 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID :308:

30

ACTGCACCCA CCCCAAGGCC ATGGCAGGGT ATGGAGATGT CATTTATCAT 50  
AAGATGGACA GATAAGCTGG ACCAATAATT AAGATTCCAG CAGAGGGTGA 100  
GGACACCCAG ATGCGCCAGG ACTGTAGGAA ATCACAATGA TGGCAACGTC 150  
TTGCCTTCCT GGGGACAGGG AGCCCTATTC AAANANAGTC ACATCTGAGG 200  
AGCCGGGGGT TATAACATCA AGTCTGTCCT TGACCTCACA AAGCCAG 247

35

## (2) INFORMATION FOR SEQ ID :309:

40

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 base pairs

168

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :309:

AGGTAAGGTT GTCACGTGGA ACAACTGATA AAGGTCAGCT ATATATGTAG 50  
10 AGCTATATAT GTGAGTCACA AGGTGTGTGA CATACGTGTA TACGTATAAT 100  
ATGCGTT 107

15 (2) INFORMATION FOR SEQ ID :310:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 114 base pairs  
(B) TYPE: nucleic acid  
20 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :310:

GGAAGACCTC GCTGGACATC CTGCAGGGCC ACATGGTGGC TCTGCTTGTG 50  
ATTCTGGGGT CCACCCTCTC CAGTCAAGAG AACCCCGTC GGGTTTAATG 100  
30 TATCAGGAAA GAGA 114

(2) INFORMATION FOR SEQ ID :311:

35 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 237 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
40 (D) TOPOLOGY: linear

169

(xi) SEQUENCE DESCRIPTION: SEQ ID :311:

	ATGGCAAATA GGAAGAAGCT CAGTATCCTC CTCCCACCAT AACCCCACTC	50
5	TCCACTGCCT CCTGGACCAT AGTTTCCTCC ACTATACGGT CCCCCCATGT	100
	TCCTGCTACC ACCAAAGTTT CCACTCTTTA TCGAACCGTA TTAGAAGGTC	150
	GCTGGTTATA ATTTCCAAAA TATGTAATTT CCACTTCCAA ATCCTTTATA	200
10	GTTGTCATAA CCACCTCCGT AGCCCCCACC CTGTTGC	237

(2) INFORMATION FOR SEQ ID :312:

15	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 147 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear
20	

(xi) SEQUENCE DESCRIPTION: SEQ ID :312:

25	TNNTCCACAA CAGNGGGACT ACTGAAGACT AGAGAACGCC TCTGTGNGAG	50
	TGGTGCAGAC AAAGACCTCA CTAAAGTGNG CTTAACAGAG TACTAGAGGA	100
	GAGAACTTGG CAATAGCAAG TACAGACAAC TATGTGAGAA ATACTGC	147

30

(2) INFORMATION FOR SEQ ID :313:

	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 151 base pairs
35	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :313:

170

CACAACAGNG GGACTACTGA AGACTAGAGA ACGCCTCTGT GNGAGTGGTG 50  
CAGACAAAGA CCTCACTAAA GTGNGCTTAA CAGAGTACTA GAGGAGAGAA 100  
5 CTTGGCAATA GCAAGTACAG ACAACTATGT GAGAAATACT GCTCCCAAAG 150  
G 151

## (2) INFORMATION FOR SEQ ID :314:

10

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 287 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
15 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :314:

20

GAAGGTTGTA CGTGGACACT ATAAAGGTCA GCAAATTGGC AAAGTAGTCC 50  
AGGTTTACAG GAAGAAATAT GTTATCTACA TCGAACGGGT GCAGCGGGAA 100  
25 AAGGCTAATG GCACAACTGT CCACGTAGGC ATTCACCCCA GCAAGGTGGT 150  
TATCACTAGG CTAAAACTGG ACAAAGACCG CAAAAGATC CTCGAACGGA 200  
AAGCCAAATC TCGCCAAGTA GGAAAGGAAA AGGGCAAATA CAAGGAAGAA 250  
30 ACCATTGAGA AGATGAGGAA TAAGTAATTN ATATANA 287

## (2) INFORMATION FOR SEQ ID :315:

35

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 183 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
40 (D) TOPOLOGY: linear

171

(xi) SEQUENCE DESCRIPTION: SEQ ID :315:

50  
GGAATCAAAC GNCTCTATAA TGAAGATAAT GTTCAGAAAA CGTGGGTTCT  
5 GTGGTGACAC TGATTTATCA AGACAAGAGG GACATGCTTC CCCTTGTTCA 100  
CCTTTGCAGC CTGTTTCTGT CATGTAGTTT CAACAAGTGC TACCTTGAGT 150  
GTAAACTAAG GTAGACTACT CTGNGAATAA GAA 183

10

(2) INFORMATION FOR SEQ ID :316:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 135 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :316:

50  
GGAATGAATC AAACGNCTCT ATAATGAAGA TAATGTTTCAG AAAACGTGGG  
25 TTCTGTGCGT GCACTGATTT ATCAAGACAA GAGGGACATG CTTCCCCTTG 100  
CCACCTTTGC AGCCTGTTTC TGTCATGTAG TTTCA 135

30

(2) INFORMATION FOR SEQ ID :317:

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 187 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :317:

CGTTTGAAAT TCATCCCAAC TGTAGGCTGA GTGACCTGAA GTTGACAGAC 50

172

TGCCGAAGTC CAAAAGCTTC AGCATTTCTT TAGTGTTCAGG ATCTACTTCA 100  
ATAATNNTGA TCCAAGGCTG AGACCTCAGA AACATAATGC TCTCCTTTCC 150  
5 CTATNTTTTC TCGGCTTGA TGGAGATACC TTTACTG 187

## (2) INFORMATION FOR SEQ ID :318:

## (i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 268 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

## (xi) SEQUENCE DESCRIPTION: SEQ ID :318:

20 TCCCAGGAGA AGGAACTTTG AAATTCATCC CAACGTAGGC TGAGTGACCT 50  
GAAGATTGAC AGACTGCCGA AGTCCAAAAG CTTCAGCATT TCCTTAGTGT 100  
CAGGATCTAC TTCAATAATN NTGATCCAAG GCTGAGACCT CAGAAACATA 150  
25 ATGCTCTCCT CCCTTNCTTT TCTGCGCTTG ATGGAGATAC CTTTCACTGT 200  
GCCTCTCTGA ATCGTTTCAT CAGATGCTGA CGTAACCTGC TATTTGTTGN 250  
AGCTTTCNGT TGNNNTAA 268

30

## (2) INFORMATION FOR SEQ ID :319:

## (i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 138 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

## (xi) SEQUENCE DESCRIPTION: SEQ ID :319:

173

ACTGCACCCA CCCCAAGGCC ATGCAGGGTA TGGAGATGTC ATTTATTATA 50  
AGATGAACAG ATAAGCTGGA CCAATAATTT ACAGATTCCA CAGAGGGTGA 100  
5 GGACACCCAG ATGCGCCAGG ACTGTAGGAA ATCACAAT 138

## (2) INFORMATION FOR SEQ ID :320:

(i) SEQUENCE CHARACTERISTICS:  
10 (A) LENGTH: 118 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

## (xi) SEQUENCE DESCRIPTION: SEQ ID :320:

AAATGATGAT AAATTCATCC TCTTCTGCTC TTAAAATTTT ATAAACCTCA 50  
20 GGCTCTGGAG AAACAAGTTG TTCTGTTGGG CCCTTGCCAT CAACACACTT 100  
GTAATCATAC TTCCCCCA 118

## 25 (2) INFORMATION FOR SEQ ID :321:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 160 base pairs  
(B) TYPE: nucleic acid  
30 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## 35 (xi) SEQUENCE DESCRIPTION: SEQ ID :321:

AGAACAGTTG AAGGTCTGAG GTGTTGAGAG GCAAATGGGG TCTCTGGGTG 50  
GATCCTGGTC CTGTCAGCAG GCCTGGACTT GTTCAGGATG GACTGGTGGC 100  
40 GTTATAAAGG GCAGATCAGG GTGCCTGTCC CTTGGCATGT CCCTTAAGAT 150

174

TTCCTTTTCC

160

## (2) INFORMATION FOR SEQ ID :322:

5

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 281 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :322:

15

AGGAGGGAGT TAATCCAAAC CACACAATGA AGTCTTCAAA CCACCNCCCG

50

AACAGGGCTG CTGATTGTTT CTTTCACTTT TGNGGTGACC TTGAGCTCCC

100

TTAAAAAAA AACTTGGAGA ATCACAACG GCAATGCACC GCAGTTCTCG

150

20

AACTACACAA GCATAGTCTG ACTAAGTCAC ATGTGTTTCC ATATCAACTT

200

GTTTGACAGG GCGACCTACT GCAAAGCAGG CTCAGTTACC CCACCAGTCA

250

25

ACCCCTGGG AGTATAATNN TCTCCATANA A

281

## (2) INFORMATION FOR SEQ ID :323:

30

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 99 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

35

## (xi) SEQUENCE DESCRIPTION: SEQ ID :323:

GGAATTTTCT CAAAGAAAAC GCAATAGCCA ATTGGAACCT ACTNTANCGC

50

40

ANTTTATNNN GTCTTCTTTA ANNTAGAGTG ACTTACTGAT TTATTATTG

99

175

## (2) INFORMATION FOR SEQ ID :324:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 167 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :324:

GGAATTTTCT CAAAGAAAAC GCAATAGCCA ATTGGAACCT ACTNTANCGC 50  
ANTTTATNNN GTCTTCTTTA ANNTAGAGTG ACTTACTGAT TTATTATTGA 100  
CACNNGTCCN NNGCNCNAGN TTACCATCCT TATGTGAATA CTNCAAGGGA 150  
TTGCCCCGCGT TTTTAGG 167

## (2) INFORMATION FOR SEQ ID :325:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 160 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :325:

TGATCCAACCT CTCCTGTGT GAAAAGAAGA ATGATGGCAG GAAGAACATA 50  
AAGACTTTAA AACTCCTAGC CGGGGTTTGT CGGACTCTTT GNCAGTAGTG 100  
ATTTAGCCAA CCAGGCAACA GAGATACGAT CTAATCTCCT CGCCCCTCTT 150  
TCGGGTCGCG 160

## (2) INFORMATION FOR SEQ ID :326:

176

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 124 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :326:

10

GGAAGGGGTG TTGTTTGATA GACATTATCT GTGGCTGGGT CTTTCTGGCT 50

GATGAGAGAC ATGTAGATTA TGTGAAGCAA GTGGCTAGAA GATGAGAGAG 100

AACATGAGAG AGCAGAGTGC TCTC 124

## (2) INFORMATION FOR SEQ ID :327:

## (i) SEQUENCE CHARACTERISTICS:

20

(A) LENGTH: 253 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID :327:

AGCCTAGTTT GAACATCCTC ATCCCNGTGT TAGACCGGAT CCGATATACA 50

GAGTCTTAAG GAAATCGCAT CAACGTGCCT GAGCAGTCGG CTGTGACTCT 100

CGACAATGTA ACTCTGCAAA TCGATGGAGT CCTTTACCTG CCATCATGGA 150

CCCTTACAAG GCAAGCTACG ACGCGAGGAC CCTGATATGC CGTCACCCAG 200

CTAGCTCAAA CAACCACGAG ATCAGAGCTC AGCAAACCTCT CTCTGGACAA 250

AGT

40 253

## (2) INFORMATION FOR SEQ ID :328:

177

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 200 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :328:

10

GAACCTCTGG GCTCTCATCC TCTCCTATTG ACAGTGAAGC CCATGGCAAA 50  
TAGAAGAAGC TCAGTATCGG CTCCTCCAC CATAACCGCG TTNAAATCGC 100  
CTCCTGGACC ATAGTTTCCT CCACCATAAG TCCCCCATG CTCCTGCTAC 150  
CACCGAAGTT CCCACTCCTG NGCGAACCGT AGTTAGAAGA TCGCTGTTAT 200

## (2) INFORMATION FOR SEQ ID :329:

20

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 280 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID :329:

30

TGACCTGATC ATCCTGAAAA ACTTTATGGG GGAGAAAGGT CAGCAGCTTC 50  
TCTTTCTTTT NTCGAAAATN ATAAACTGC GTATTCTACT TTATATTTAA 100  
TGTAAGGAAG AAAATATACA AGCCCATATT TACATCGTAT TTCTATTAAG 150  
AGCAACAATA GTTCATATGT TCATGTTTGC TACTATCACA ATNCAACATA 200  
TGAACACAGA TCAGCTCTAT ACCATGAATA CTGCTGGAAG TGATGGTTTA 250  
GGATTACCAA CTCACTGCTG CCATGACCGA 280

40

178

## (2) INFORMATION FOR SEQ ID :330:

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 268 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :330:

CCTGAAAAAC TTTATGGGGG AGAAAGGTCA GCAGCTTCTC TTTCTTTTNT 50  
15 CGAAAATNAT AAAACTGCGT ATTCTACTTT ATATTTAATG TAAGGAAGAA 100  
AATATACAAG CCCATATTTA CATCGTATTT CTATTAAGAG CAACAATAGT 150  
TCATATGTTT ATGTTTGCTA CTATCACAAT NCAACATATG AACACAGATC 200  
20 AGCTCTATAC CATGAATACT GCTGGAAGTG ATGGTTTAGG ATTACCAACT 250  
CACTGCTGCC ATGACCGA 268

25

## (2) INFORMATION FOR SEQ ID :331:

## (i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 170 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

## (xi) SEQUENCE DESCRIPTION: SEQ ID :331:

TCGCAGGAGA AGGAACCTAT ACACCCTTTA TAGAGCTTTA AATCGACTGT 50  
AGAGTTTTGT GGTCTTCCAG TCCCAAATGT TTAATTTTCC ATTTGCATTN 100  
40 TGAAATCACA TAACTCATGT CTGAAAAGTC CACCTGACAA GCATACCTGC 150

179

TACCATATGC CCTTAAAAAT

170

## (2) INFORMATION FOR SEQ ID :332:

5

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 223 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :332:

15

TCGCAGGAGA AGGAACCTAT ACACCCTTTA TAGAGCTTTA AATCGACTGT

50

AGAGTTTTGT GGTCTTCCAG TCCCAAATGT TTAATTTTCC ATTTGCATTN

100

TGAAATCACA TAACTCATGT CTGAAAAGTC CACCTGACAA GCATACCTGC

150

20

TACCATATGC CCTTAAAAAT NNGGNNNNNG NNNNGGNTGA ANGTTCTGT

200

GTTCCAAAAA TANTAAGATTT GTT

223

25

## (2) INFORMATION FOR SEQ ID :333:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 132 base pairs

(B) TYPE: nucleic acid

30

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

35

## (xi) SEQUENCE DESCRIPTION: SEQ ID :333:

AGACAATTGG CGGCATCCTC GTAGGCTTCA CTAAGTCCCA CAAGTTCTTC

50

TGGTTTCATT TCGGTTATTT TTTGCAGCCA ATTCTCTCCA TGTTTGGCAG

100

40

TCACAAGGCT CATGTGCTTC ACCAAGGCAC TC

132

180

## (2) INFORMATION FOR SEQ ID :334:

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 235 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :334:

AAGTTGTTCA TGGNAGGCAT TTATCCTNTC AATAATNCAA ACGAGGCTTC 50  
15 TGGGAATAACC AGTGCCCCAT TCCATCAGAG TCTTTGCGCG ACTAAAGCCT 100  
CCATNTTTGC CAATTTCAAT TGTTTGGGAT TCTAGCACTC CTTACCNGCA 150  
GTAATGCCCT TGCTGCAGAC AACAAACACCT GGA CTGNGAG ATGGACCAAT 200  
20 TCTCAATGGC AATCCAGGGA AAGAGTGATC CTTCT 235

## (2) INFORMATION FOR SEQ ID :335:

25

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 169 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :335:

35 ATGCCCCGCAC CATCCGCTAC CCCGATCCCC TCATCAAGGT GAATGATACC 50  
ATTGAGATTG ATTTAGAGAC TGGCAAGATT ACTGATTTC TCAAGTTCTGA 100  
CACTGGTAAC CTGTGTATGG TGACTGAGGT GCTAACCTAG GAAGAATTGG 150  
40 GNGATCACCA ACAGGAGAG 169

181

## (2) INFORMATION FOR SEQ ID :336:

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 193 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :336:

ATGCCCCGCAC CATCCGCTAC CCCGATCCCC TCATCAAGGT GAATGATACC 50  
15 ATTCAGATTG ATTTAGAGAC TGGCAAGATT ACTGATTTCA TCAAGTTCGA 100  
CACTGGTAAC CTGTGTATGG TGA CTGAGGT GCTAACCTAG GAAGAATTGG 150  
GNGATCACCA ACAGGAGAGG CACNCTGNAN TCTTTTGGCN NNG 193

20

## (2) INFORMATION FOR SEQ ID :337:

## (i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 307 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :337:

CAAAAGTCAT CCACAAGTTC TTTGTCTAGG ACTTCTAGCT GCTCAGACCC 50  
35 TCAGGGTCTT TGGATTGTTA CCAAAGTCTG TCAAACAGAC CAGTAGTTTA 100  
ATACCTGTAC AGAAAAATGT TTCTATTATG CTTCTAGTAT CTAGAAATTG 150  
CTTGCTACAG CATGGAGGTG GTTCTGCCTT TCCCTGGCTC CTCACACTCT 200  
40 CATCTGCAGG ATTCCCAGCT TTGCTCAGTC TTCATGCCCA CCAGAGGCAA 250

182

AAAGGCAAAC TAAAACTGTC ATGCAGTGGT AGGTTTGAAA TNAGCTGCTG 300

CATCATG 307

5 (2) INFORMATION FOR SEQ ID :338:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 305 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :338:

AAAAGTCATC CAQAAGTTCT TTGTCTAGGA CTTCTAGCTG CTCAGACCCT 50

20 CAGGGTCTTT GGATTGTTAC CAAAGTCTGT CAAACAGACC AGTAGTTTAA 100

TACCTGTACA GAAAAATGTT TCTATTATGC TTCTAGTATC TAGAAATTGC 150

TTGCTACAGC ATGGAGGTGG TTCTGCCTTT CCCTGGCTCC TCACACTCTC 200

25 ATCTGCAGGA TTCCCAGCTT TGCTCAGTCT TCATGCCCAC CAGAGGCAAA 250

AAGGCAAAC TAAACTGTCA TGCAGTGTA GGTGAAAT NAGCTGCTGC 300

30 ATCAT 305

(2) INFORMATION FOR SEQ ID :339:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 101 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :339:

183

AATATAAAGA GGAAATGGCT CNTCACCTTC ATAATACCAA GACCTGCTCA 50

ATTTAAGATG GCCCTTGACA TTGAAATCGT ACCTACAGAA AGCTTGNAAG 100

5 G 101

(2) INFORMATION FOR SEQ ID :340:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 113 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :340:

GTGCGAGGAG AAAAAAGTCG TCACGTCATG CGAGTGCGCA GGGGGCGTGG 50

20

AGAGTAGCAG TAGAGCAACA AAGTACATAT AGGACAGTGC AGCGAGGACA 100

AGGACTTCCC GCA 113

25 (2) INFORMATION FOR SEQ ID :341:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 209 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :341:

ACACAAATAA CTACATNTAC GCAATATAAT NTTTAAAAAT CCAAAGCAAT 50

ATAAAAGAGC AGAGCTAGGA CTGAACAGAA CATTTTGGTG TATAACCGGC 100

40

AGCTCAAAAT CGCCAGCTGA TTGGAGTAAA ACTGATTCTA AGCGTATTAA 150

184

ATACGATTGA TTGTTTCCAT CACTAAGGGT GCCTATGAGT TTCTGAACCA 200

TTTCTAGGG 209

5 (2) INFORMATION FOR SEQ ID :342:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 252 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :342:

GATCAANCAA AGCACAGGGA AAAGAGGCAA AATGATCACA GAAATCCGTT 50

20 TTTTAGACAG GTGTGACTTA CACTAACGAA AAAGAAAAAC ACATGAATAA 100

GCTTTTAATC TTCATTTTNN NNTTTTGTNA TGGTAGGCTG AGATGCTTTT 150

AAATGTGATG TTATAAGCCT AAGGCAGCTT GACTGCAGCA ACAAGTTTTT 200

25 TACCCTCCTT GGCAAAGCAG GTCTCCTTAT GTAGCCTTGC AGCACTTCTC 250

TA 252

(2) INFORMATION FOR SEQ ID :343:

30

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 258 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID :343:

GATCAANCAA AGCACAGGGA AAAGAGGCAA AATGATCACA GAAATCCGTT 50

185

TTTTAGACAG GTGTGACTTA CACTAACGAA AAAGAAAAAC ACATGAATAA 100  
GCTTTTAATC TTCATTTTTN NNTTTTGTNA TGGTAGGCTG AGATGCTTTT 150  
5 AAATGTGATG TTATAAGCCT AAGGCAGCTT GACTGCAGCA ACAAGTTTTT 200  
TACCCTCCTT GGCAAAGCAG GTCTCCTTAT GTAGCCTTGC AGCACTTCTC 250  
TACAAAAC 258

10

(2) INFORMATION FOR SEQ ID :344:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 227 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :344:

GAAGGAACCA GTGACCAGTC ATCCCCAGAG ATAGATGAAG ACCGGATCCC 50  
25 CAACCCACAT TCAAGTCCAC TTTGCAATGT CTCCACGGCA ACGGAAGAAG 100  
ATGACAAGGA TCACACCCAC AATGAAAGAG CTCCAGATGA TGGTTGAACA 150  
TCACCTGGGG CAACAGCAGC AAGGAGAGGA ACCTGAGGGG CCGCTGAGAG 200  
30 CACAGGACCC AGGAGTCCGC CCACCTG 227

(2) INFORMATION FOR SEQ ID :345:

35 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 188 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

186

(xi) SEQUENCE DESCRIPTION: SEQ ID :345:

AAATAAAAAA TAAGGTCCAA GCCAATGCCT AACAGATAAT AAGAGCTCAG 50  
5 TAAATGTTGA TTGAATACTA ACAAAGTAGT GAAAGCAGAC GACACAGTAC 100  
CTGGCACACT ACTAACTGT AAATGTTTTT AAATCTGAAT CTGTAGAATT 150  
CTGTAAGGTT TTATGTAATA TGANGTCATT AGCTATCA 188

10

(2) INFORMATION FOR SEQ ID :346:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 262 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :346:

AAATAAAAAA TAAGGTCCAA GCCAATGCCT AACAGATAAT AAGAGCTCAG 50  
25 TAAATGTTGA TTGAATACTA ACAAAGTAGT GAAAGCAGAC GACACAGTAC 100  
CTGGCACACT ACTAACTGT AAATGTTTTT AAATCTGAAT CTGTAGAATT 150  
CTGTAAGGTT TTATGTAATA TGANGTCATT AGCTATCATG NCTCTGGATT 200  
30 NNCTNNNAGG TTTTAAGATG GAGCATCTGN GNATGTCAGC CCGTCCTATC 250  
TAGAAGTGNA AA 262

35

(2) INFORMATION FOR SEQ ID :347:

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 159 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

187

## (xi) SEQUENCE DESCRIPTION: SEQ ID :347:

5 CTCTGTTTT CAAACGCCCA TGTGTGCTAT ACTACAACTC TTCTCGAGTC 50  
TGATCAATTT GCAGTAGACC ATTTTAGTTC TTACGACGTT AATAACAAAC 100  
ACTTCAACAT CANTGCTCCA ATCTGAAGTT CTTGTTGCAT TGTAAAAGA 150  
10 AATNTCTAA 159

## (2) INFORMATION FOR SEQ ID :348:

## (i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 283 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID :348:

TCGCAGGAGA AGGAAGCTGC ATGCACTTGA AAGGCATGGC CTGTCTCCTC 50  
25 ACTGAGTGCA AGGTCCATCG ACCAAAGCCC TGTTCTGATC AATAACATCT 100  
ACAATCGCAC CAATTTTCCG GCATGAGGTC CAAAGGAGAC ATAGGCCACC 150  
30 CGGCCAACCT CCACGAAGCG CCTGAACACC ATGCGCTTCC CGGGACCCTC 200  
TGGGAGCCGT TCGCNCCTCA GCTTCCCAGC GAGGTGGAGG TCGAGCGGCA 250  
TGGNCGACGC CCCGGAGCCC ACAACAGTAA GAC 283

35

## (2) INFORMATION FOR SEQ ID :349:

## (i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 169 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :349:

5 CAGAAAGGAG GCATTGAGCA AAAACTAGGA AAATCTGAAT AAACNGTGGA 50  
CCTCGCTTGG TTAATATATT TANACTGGTG ACTCATTTTA AAACTTTCCC 100  
GGGCGCGATG GCTCATGTCT GCAATCCCAG CACTTGNGAG GCTGAGCGGG 150  
10 TGGATCACCC AGGTCAGGA 169

## (2) INFORMATION FOR SEQ ID :350:

15 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 175 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear  
20

## (xi) SEQUENCE DESCRIPTION: SEQ ID :350:

25 GAAGNAACCA GTACCAGTCA TCCCAGAGA TAGATGAAGA CCGGATCCCC 50  
AACCACANT TAAGTCCACT TTGCAATGTC TCCACGGCAA CGAAGAAGAT 100  
GACAAGGATC ACACCCACAA TGAAAGAGCT CCAGATGATG GNGAACATCA 150  
30 CTTGGCAACA NCACAGGAAG GGACC 175

## (2) INFORMATION FOR SEQ ID :351:

35 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 206 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear  
40

189

(xi) SEQUENCE DESCRIPTION: SEQ ID :351:

AAATAAAAAA TAAGNACCCA ACCAATGCTA CAGATAATAA GAGCTCAGTA 50  
5 AATGTTGATT GAATCACTAA CAAAGATAAA AGCAGACGAC ACAGTACCTG 100  
GCACACTACT AACTGTAAAT GTTTTAAAT TGAATCTGTA AAATTTGTAA 150  
GGTTTTATGA ATATAATATT ATTAATATT ATGTCTCTGA ATTTTNNNN 200  
10 NAGGCT 206

(2) INFORMATION FOR SEQ ID :352:

15 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 76 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear  
20

(xi) SEQUENCE DESCRIPTION: SEQ ID :352:

25 AGACATACTG TAGTGTCTAA ATAATATTTG TCNGAAGATA ACAATTATGG 50  
GACTTTAAAG CCGACAGTGA AATTAT 76

(2) INFORMATION FOR SEQ ID :353:

30 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 245 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :353:

40 ACATTTGGCC CTCAGACTGT AATTTCATA CTACTNTGAC TGATACTAGA 50

190

TGACCTGGCT GCCTAGGGGC TGTGCTGGTC TGATTTTTTG TGAGACAAAA 100  
ACCACTCTAA ACCTCCTGGT GCACTGAGGC TGTACACACC GNCAGAACAG 150  
5 GGCACTGCGT TAAAAAGTTT CTGACCAAGT GGTGACAACA GAGGNCAAAC 200  
GTAAGGCTGT CTGGATAAGT TGAACCTNGC TGANCGGTAG CACCA 245

## (2) INFORMATION FOR SEQ ID :354:

10

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 179 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
15 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :354:

20

GGAATCTGTG CCACACAGCT GCACACGACT ACTGGCCAAA GGACAGCCTC 50  
AGAACATCAT GAGCTGGCGT GACCTCATGA TGNNCCTCAN TGCTGTGGGG 100  
25 CTTCTGCTNG AGGCCAGCAG AGGCTCGTAT GACTACCTGT NAGACCTGCT 150  
CTTTGGGTTG AGACTTTTCA GNGACAACT 179

## (2) INFORMATION FOR SEQ ID :355:

30

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 139 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
35 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :355:

40

AAGGAACGNA TGACTTTCCA TCCCTTGAAC CAAGGCATGT TAGCACTTGC 50

191

TCCAGCATGT TGTCAACATT TCAACAGAAA TCGCACAAAT GCTACTGTGC 100  
AAGGTGCAGC CAATTTTNTT GTAAGTGTGA TTTCTTACG 139

5 (2) INFORMATION FOR SEQ ID :356:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 100 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :356:

TCCAGGAGAA GGAAACTTC CACTTATAAC TGTNTCAGCC TGACTATAAT 50  
GAAGAGACTA GCAACACCTC CTGAACACAA GCCTANTGAG CCCAGTCTTT 100

20

(2) INFORMATION FOR SEQ ID :357:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 137 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :357:

AGAAGGAAAC ACCAAAGAAA CATCCAAGCA ATAAAGTGGA AGACTAACCA 50  
35 AGATTGGAC ATTGGAATGT TTAAGTTAT TCTTTAAGAA ACAACTACAA 100  
AAAGAAAATG TCAACAAATT TTTCTAGCT AACTGAG 137

(2) INFORMATION FOR SEQ ID :358:

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 228 base pairs

192

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :358:

10	AAGGAACAAG TGGGTCATTC TCACTAAGGC TGCCTGTCAC TGCAGTCTTG	50
	ATCAGCTTGT CAATTGATA CTCAGCTTT TGGTCCAAGG GACGAAGCTT	100
	TTCCAAAACC GTTCGAATCT CTACCAGTCT CAAACTGCA TCATGTCCCT	150
15	GAAGAGATCC TCCTGAGGCT TTGTCCAGAA TGAGGTGGGT CAAATNNANG	200
	GGNACATGAG CAGCAGCTGN TCTTTAAC	228

## (2) INFORMATION FOR SEQ ID :359:

20

## (i) SEQUENCE CHARACTERISTICS:

	(A) LENGTH: 248 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
25	(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :359:

30

	CAGGAGCAAG GAGGCCATTT TGCTGAGCTC TCACAGCTGC TAGAGATGCT	50
	CAATGACTCC CAATACAACC CAAAGAGACA AACGCTTGTT TTTTCTGCCA	100
35	CACTCACCCCT GGTGCATCAG CTCCTGCTCG AATCCTTCAT AAGAAGCACA	150
	CCAAGAAAAT GAATAAAACA GCCAAACTCG ACCTTCTTAT GCAGAAAATT	200
40	GGCATGAGGG GCAAGCCCAA GGTCATTGAC CTCACAAGGA ATGAGGCC	248

## (2) INFORMATION FOR SEQ ID :360:

193

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 253 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :360:

10

AGGCACCTGT GGAGCCATCC TCCTTGTTTT AATCGTCCTG CTGCTGCTGC 50

CGTTCCGTGT CGCGTCGCCC ACATGACCCT GAGGTCGCAA TGATGAGTCC 100

15

TCTCTGGTCA GACACCGCTG GAAATGAATA CCAGGCCTGA CCTCAAGCAA 150

CCATGAACTA GCTATTAAGA AATACANNGG NAGGGCGGCA GCCGGATCGT 200

GNNGGCGTTT NTCTGNGCCG CCCGTCTCAA TCTNTGTTCT GCTTCCAGAT 250

20

GCC 253

## (2) INFORMATION FOR SEQ ID :361:

25

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 154 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :361:

35

GAGAACCACG GGCTCCATCC TGGCCTCCTG TNCACCTTCG AACAGATGCG 50

GATTAGCAAG CAGGAGCACA CGAATCAAGC CCCTCCAGCC ACCAAATTTT 100

CTAAACNNGC TNGGCNATGT CGTAGTTNGT TGTCAGTNGA TCGGTAGAGA 150

40

TAAT 154

194

## (2) INFORMATION FOR SEQ ID :362:

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 168 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :362:

GAGAACCACG GGCTCCATCC TGGCCTCCTG TNCACCTTCG AACAGATGCG 50  
15 GATTAGCAAG CAGGAGCACA CGAATCAAGC CCCTCCAGCC ACCAAATTTT 100  
CTAAACNGGC TNGGCNATGT CGTAGTTNGT TGTCAGTNGA TCGGTAGAGA 150  
TAATCCTGNC CACGCCCT 168

20

## (2) INFORMATION FOR SEQ ID :363:

## (i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 198 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :363:

AAGGGATAAA AGGAAGCTTT GNCACCACTC TACCATCAAA NNGGAATTGA 50  
35 ACATTCCCAT TAAGGCAGTA AAACAAAAGC CAATAGCAAA CATGNATTTT 100  
ATTCAACCAT TGATAGATCT CTGCCGTTAT TCTTCAGTTT CTCTTCTCGT 150  
CTCTCTATTT NTTTCTCTGG TTGTCGACCA GCTGACTNTG NCATCGTT 198

40

## (2) INFORMATION FOR SEQ ID :364:

195

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :364:

10

TTATACAAGT CAAACTTGGG AGGTCATAGT AAGCATACCT ATGCTGAGAG 50  
AAAAGCATCA AATCCTCCGC GACACATCTA GTTCATCGTA ACAAAGCAAC 100  
TCGTACACTT TCAAGTTTAA A 121

15

## (2) INFORMATION FOR SEQ ID :365:

## (i) SEQUENCE CHARACTERISTICS:

20

- (A) LENGTH: 211 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID :365:

30

GGTAAGTTGT ATTTGGGCCA GAATTTTAAA GAGCACTATT TCGACATTAA 50  
AATGTATTCT TCTCGTATTA ATGCCTACAT CTTCAGAGTT TTCAATGCTT 100  
TCTAAAAGTT TCCTCTTTGG AAAGAAGAAA TCTGAAAGAC CTATCATGCC 150  
GTTCTTCCTG GCGTCTATAT TTCCTTTAGA GAGGCAAGGT AGGATTCCGT 200  
CTCCAAGGGA G 211

35

## (2) INFORMATION FOR SEQ ID :366:

40

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 285 base pairs

196

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :366:

10	CGGCTACAGC ATCACATCCA CTAAATGCAC AGTTGTTGAA GTCACGCCCT	50
	GCCAGACCTC TACTACCACA TTGTTCCCTC CGGTGACCAG TTTGTCCGTC	100
	ACTGTCAGGA GAATGNCCCG TGTCGAATCA TCGATCTCCA TCCGAGCCAA	150
15	AAGTTTTCCA TATGCTGAAA TTACTGAATT GCCCTCGTTT ATAGTATATG	200
	ATACAGTGGC CTTGTTGGA GGCAGATATC AAGCATGGGG ATAAGCAGTT	250
20	TTCTGGTCCT TAAGGGCTCT CAGCAAATCT CCGTG	285

(2) INFORMATION FOR SEQ ID :367:

(i) SEQUENCE CHARACTERISTICS:

25	(A) LENGTH: 149 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :367:

	GACACTGAGG CAGCTACTGA GAAGGGCAGA ACATGTCTCA ATCCATAGAG	50
35	GTCTTGGCAG GCGAACCAG AGAGACTTGC AGTACGTGAG AAGATGGAGA	100
	ACCAAATAAA AGGACTGGAG TCCAGTTCAA ACAAGGAGGG AGTGGTAGT	149

(2) INFORMATION FOR SEQ ID :368:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 137 base pairs

394

CTATGACCCA GCCATGGGAT CAGGCTCATT GCTTTTGACG ACTGCTTCAT 100  
ACATGAAGAA TGATGGTGTT CGTGGGGCCA TTAAGTACTA AGCCAAGAAG 150  
5 TTATCACGAC AACCTATAAC TTGGGCCGAA TTAAGTTGAT GATGCACGGG 200  
GTGGAGTATA ACGATATCAA TATCCATAAT GCAGATACCT TGAGTTCAGA 250  
CTGGC 255

10

(2) INFORMATION FOR SEQ ID :787:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 206 base pairs  
15 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :787:

CATTGAAAAG TGCCTGAAAA ATGGTAAATT CTTAAATGTG TGTGAGATTG 50  
25 TCAGAATCAA CAAACTAGG TTGGTTAAAC ATATCTCTGG TACATCAAGG 100  
GGCATGATAC AAACCACTCT AAAGACTGTT TATAAAGGAG AGAGCTGGCG 150  
ACTTATTTTTT ATTTTTTTTT TTTTGGACAG ACTCCCTTTG TCCCCAGGCC 200  
30 GGAGTG 206

(2) INFORMATION FOR SEQ ID :788:

35 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 260 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
40 (D) TOPOLOGY: linear

393

TGAGTATTCG TACAAGAAGC GACCAATCTT ACCGGCATCA AGTGC

295

## (2) INFORMATION FOR SEQ ID :785:

5

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 303 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :785:

15

GTGTAAAGCG AGTAGCCCCC AAATCAGTCA TCTTGGCCTG AAGATGTAAA

50

CAAGGAGGTT TGCTTCCTGC AAGATGAGTA CTTCACTGAG TTTGGTTTTTC

100

ATTTTTCCTA CACCGAAGCC ACCTCTGTCC ATCCAATGTT CATGTCTGTC

150

20

CGAGGCTGCG CAGGAGGTTA CGTCAAGATG TGGCCAATAA AGTCCAAAAA

200

GCGCTTTGAA TACTGTTCTG GGTTCACGGT GGAGATCTCC GCGCAGCCAT

250

25

GTTTAACAGT TTTTGCAGCA TGGGCAGCTT TCTTTTTTGC ATCATAATGA

300

GTA

303

## (2) INFORMATION FOR SEQ ID :786:

30

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 255 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

35

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :786:

40

TATGGCGCGG ATCCTAACGG CTGGAATGAA GATATGCCAA CGTACAGCCT

50

392

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :783:

10 CACAGCCAGA GCTTCGTCCT CAGTGACCAC AGGGCTGAGC CAGGCTCAAC 50  
CGGCTTCTGG CTCTTGTTTT GCAGAAGAAG AACTAGAAGC AAGGNGCTTT 100  
CCTCCGGGTC CCAGAGCTGT TAGTGATGGA GCCAGGCCTG GGATCCAGCT 150  
15 TTCCTGAGTT CCTGACCCCT GCTATTTTAT TAGTCAGCTC TCAGCACTTA 200  
CCAGAGGAAC AGGCAGCCTT TTGGCTACTG CCTTCAGAGA AAGAGAGATG 250  
AGAGAATTCA AATGCGTGTT GGTGTTCTG TTAGTACAAG CAGCA 295

20

(2) INFORMATION FOR SEQ ID :784:

(i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 295 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :784:

CAATAGCGAC TTCTGGTGTC AATTCGATAA TCGGCCAATG GATACTTCAC 50  
35 GTGTGTTTCA TCGTCTGTAA TAACGGCGAA TGGTGTCAC T CAGAACCAG 100  
TACCTGATGT TGTGGAATG GCAACCATTT GTGTCAAACG CACTGGTAGA 150  
ACTTCACGAT ACGCTTACGG ATGTCCATGA ACTTTTGTTT TATTTCCATG 200  
40 AACAAATTCCT TGATACCTTC TTCGTCTGAC AAAATACCTT CGTGACGTGT 250

391

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 188 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :781:

10

GAGAGAACCC ACCATAGTAC TGTCTCCTGC AGACAAGACC AACGGCAAGG 50  
CCGCCTGGGG TAAGGTCGGC GCGCACCTGG CGAGTATGGT GCGGAGGCCC 100  
TGGAGAGGAT GTTCCTGTCC TTCCCCACCA CCANNNACTA CTTCCCGCAC 150  
TTCGACCTGA GCCACGGCTC TGCCCAGGTT AAGGGCCA 188

15

## (2) INFORMATION FOR SEQ ID :782:

20

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 182 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID :782:

30

AATATTTATT TCATTTGTTT ACTACCACTT CATTTTATTT GTTTGCTGCT 50  
GCCGTTTTAT TTATTTTAC TGAAAGTGAG AGGGAAC TTT TGTGGCCTCC 100  
AACCTTTTTC TGTAGGCCGC CTTAAGCTTT CTAAATTTGG AACATCTAAC 150  
AAGCTGAAGN GGAAAAGGGG GTTTCGCAAA AT 182

35

## (2) INFORMATION FOR SEQ ID :783:

40

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 295 base pairs

390

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :779:

TCGGATTTAT	ACGGCTGTTA	GTGCTATCGG	CGTCTGGTAT	GTGTTATATA	50
TCGCCTATCG	TTTTTTGGCC	AATGGGCGTT	GGCTACGCGG	GGCAATGATT	100
10 GCCATCGTTT	TTGTTATCTT	GACTTATTTT	GTCATTTTAA	ATATTATTTA	150
ACTATTTTAC	AAATAAAGTG	GTCAAATGGG	ATATTTTGCC	AAAAATAGAG	200
15 AAAGTGTTAG	GCGGCCACAC	GCTGGAGGAA	GAGAAAGCGG	CTGTGCATGA	250
AGTTATTGCA	CCCGC				265

(2) INFORMATION FOR SEQ ID :780:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:	249 base pairs
(B) TYPE:	nucleic acid
(C) STRANDEDNESS:	double
25 (D) TOPOLOGY:	linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :780:

30

CTCAGCTGGA	CCAAATTAGT	TGAATTACTC	ACCATCAATA	AACTATAAAT	50
GGCGCCAATG	ACCAACCCGC	CAACGATTCC	CGTTGTCAAA	GAACCTAATA	100
35 ACAAGTAACC	AACCGCAGCC	CCAACAAGCC	CAACTAGGTT	TAAAAAACC	150
AAGCAAAAGG	CCAAGTGTCC	GTCGTTTATT	GGATTGTATC	TGCTCATATA	200
ACATTAAAC	TTAACCGTTG	GCACTTCTTT	CTCAGACCCG	CCGATACTG	249

40

(2) INFORMATION FOR SEQ ID :781:

389

## (xi) SEQUENCE DESCRIPTION: SEQ ID :777:

	AGATTCTGCA GTGTAATATG ACCAAATCAA ATCCGTTGTA TGATCGAATA	50
5	AGGCCGTCAT AAAGTAAGTT GAAAATTTCTG TTCTTGGCTG AATCGTGTTA	100
	AACCGTTGTA CACAACGTAG TAAAATTCAT AACCCATCTG CATACCAATC	150
	GTCAGCCGTG ATGCATTTAC TCACTTTACG TCGATGAATG TCAAACATCG	200
10	CACCTTTTCA ATGTTTACTA AAAACATAGC ACGCAATAT	239

## (2) INFORMATION FOR SEQ ID :778:

15	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 252 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID :778:

25	ACTGAACAAC GTAAGGTCTT GACTGACACT TACAAGTTGG ATGAATCTGA	50
	AATAAAGTTG GTATTGTTTG AAGCAGCCCA ACAATTTCTGA ACATGCTACA	100
	AGACCGTCGT TTGACTGACA AGGCCTTGAA GTACATGACT GACAACAACG	150
30	TCGATCTTCG CCTAGGCGCC ATGGTCACTG GTGTTGACGA AAATGGCGTG	200
	ATTTTAAAGG ATGACTCAAC TTCGCCAACT CGGTTCTCTCA TTAGGACAAC	250
35	TA	252

## (2) INFORMATION FOR SEQ ID :779:

40	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 265 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double

388

TGAAGGAAAT GACTACCTTG CACTACATGA AAAGGATATC GTTGCCATTG 50  
TGGCGTAATT TTCGTGCCGA GTGAATGTGG CGCAAACAAC TATATATCNA 100  
5 AACCGTATAT TTAAATGAA TTACTAGAGA GGAATGTAA TCATGGCAAA 150  
AGAAATTAAG TTTTAAGAAG ATGCTAGTGC TAAGC 185

(2) INFORMATION FOR SEQ ID :776:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 255 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :776:

20

ATCCAAGCCC ATACCCATCA ACAATGGGAC AGCGATTGGA TCACCAGCCA 50  
TTTCACCACA CATGGCAACA AACTTACCTT CTTAAGAGC GGCAGTAATC 100  
25 ACATCGTCGA TCAAACGCAA AATCGATGGG TTATAAGGTC GATACAAATA 150  
AGCAACCTTA TCATTACCAC GATCTGCAGC CATCGTATAA CCAATCAAAT 200  
CGTCGGTACC AATCGAGAAG AAGTCCAATC CCTTAGCAAA CTCATCAGCC 250  
30 AACAT 255

(2) INFORMATION FOR SEQ ID :777:

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 239 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 40 (D) TOPOLOGY: linear

387

GAATTAGAGG TAAAGGAATC CTAAAATAAA GAGCACAGCA GCAATCACAC 100

TCACAGGGTC CAGAGGCGTA TTCCTGGCCA TCTTCCTAGT ACTCGGTCCG 150

5 T 151

(2) INFORMATION FOR SEQ ID :774:

## (i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 299 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

## (xi) SEQUENCE DESCRIPTION: SEQ ID :774:

20 ATCTTAATGA ACATGGCATT TAAAATCCTG TAATTTCAA CAGTGAACCA 50

CAATGCCGTA TGATCTAAAG GCTGCTGAAC CACAGCGTGG ATACACTTAA 100

CTGAGCTCCT CGCTGGGTCA AAGCACTCAT CTCCGAGTCT AAAGCTACAC 150

25 ACTATGGAGC ACACAACTCT GCCTCGCGCT GACACCAGAC AAACACGGCG 200

GGAGCTGAGG CGGACAGCTA CAGGACCACG AGCATAGACC ACGGCACCTG 250

30 AGACCATCTC TACGCAAGGA CTTAAGGAAG CAAATATAAT ATTAAAATA 299

(2) INFORMATION FOR SEQ ID :775:

## (i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 185 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

## (xi) SEQUENCE DESCRIPTION: SEQ ID :775:

## (xi) SEQUENCE DESCRIPTION: SEQ ID :771:

5 GCCACCGCCG ACTCCAGGCA CTCACTCAA CTCGATCTTC AACTCTGCAT 50  
ACAAGCAGAA GCAATAAACC AATCTGATTT TCTTTTCAAT T 91

## (2) INFORMATION FOR SEQ ID :772:

10 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 177 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear  
15

## (xi) SEQUENCE DESCRIPTION: SEQ ID :772:

20 GCCTGCGCCG ANGCAATCCC TTTGACCTGA GTCTGCAGCA GGTCCCTTTT 50  
GCGCTTCCTT CCCCTCAGGT AGCCTCTCTC CCCCTGGGCC ACTCCCGGGG 100  
GTGAGGGGGT TACCCCTTCC CAGTGTTTTT TATTTCCGTG GGGCTCACCC 150  
25 CAAAGTATTA AAAGCAACTT TGCAATT 177

## (2) INFORMATION FOR SEQ ID :773:

30 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 151 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
35 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :773:

40 AACATAAGAG GAGAAAGGAA GGGACATGAG GCATACCATT CCCCCCCCCA 50

385

CTGCGGACCA GGATGCAGTG CCAGGCATGG GAGTCATTGC CCACATCACC 150

GAGAAGGACA AAATCACCAC CAGGACACTG AAGGCCCGAA TGGACTCGCC 200

5 CTGCTCCCAG AGCCCACTTT TTT 223

(2) INFORMATION FOR SEQ ID :769:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 37 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :769:

GCCAGCGCCG AAAACACACA CTTTGCTTCT TACCTGC 37

20

(2) INFORMATION FOR SEQ ID :770:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 37 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :770:

GCCAGCGCCG AAAACACACA CTCTGCTTCT TACCTGC 37

35

(2) INFORMATION FOR SEQ ID :771:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 91 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

384

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :766:

GCCAGCGCCG ACGATGCCCA GAATCCAGGA CTTGCCTAT CACTCTCCCC 50

AACAACTAG ACGCGAAAAC AGAATAAACT TCACCCAG 88

10

(2) INFORMATION FOR SEQ ID :767:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 91 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :767:

GCCACCGCCG ACTCCAGGCA CTCACTCAA CTTGATCTTC AACTCTGCAT 50

25 ACAAGCAGAA GCAATAAACC AATCTGATTT TCTTTTCAAT T 91

(2) INFORMATION FOR SEQ ID :768:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 223 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :768:

GCCTGCGCCG AACAAATATA CAGAATGCGC GAGTCCCTCT GGAAGCCCAA 50

40

CATGGATCCG GATCACCTGT TTGAAACCAT CTCCAAGCC ATGCTGAATG 100

383

CGGATAGTCA CACTCCCTGC CGA

223

## (2) INFORMATION FOR SEQ ID :764:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 70 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :764:

15 GCCAGCGCCG AGGTTGCATA TTTCTAGGCG CAGGTATATG ATTGCCATAT 50  
AATAAAAATC TGAAAACACC 70

## (2) INFORMATION FOR SEQ ID :765:

20

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 118 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID :765:

30

GCCAGCGCCG ACCGCCCAA AAATACTCCC ACCGGGATCA GGGCGATTAA 50  
TGAAGACTCA ACGGGGACTA AAAAGGGGCC CCAAAAAAAAA CCAAACCACC 100  
TTTCTACGTA CCGTATAG 118

35

## (2) INFORMATION FOR SEQ ID :766:

- 40 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 88 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double

382

## (xi) SEQUENCE DESCRIPTION: SEQ ID :761:

10 GCCAGCGCCG AGGTCGCATA TTTCTAGGCG CAGGTATATG ATTGCCATAT 50  
5 AATAAAAAC T GAAAACACCC C 71

## (2) INFORMATION FOR SEQ ID :762:

10 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 88 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

## (xi) SEQUENCE DESCRIPTION: SEQ ID :762:

20 GCCTGCGCCG ACGATGACCA GAATCCAGAA CTTTGCCTAT CACTCTCCCC 50  
AACAACCTAG ACGCGAAAAC AGAATAAACT TCACCCAG 88

## (2) INFORMATION FOR SEQ ID :763:

25 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 223 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :763:

35 GCCTGCGCCG ACAAACAAAA CCTGGAGGCC ATTCTGCACA GCCTGCCCCGA 50  
GAACTGTGCC AGCTGGCGGT GAGGGCTGCC CAGATCCCCG GCACACACTC 100  
CCCCACCTGC TGTTTACATG ACCCAGGGGG CGCACACTAC CCCACAGGCG 150  
40 CGCCCATACA GACATTCCCC GGAGCCGGCT GCTGCGAACT CGACCCCCTG 200

381

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :759:

GCCACACCAG ACTTTCGACC CCCCAACCCT CTGAGGAAGA TGGGGGCAAG 50  
AAGATCACGC TCCCCGCGCTG TTCCCCCGCC GCTTTTCTCC TCTCTTCTCT 100  
CTTCGCTCTC AGCTCCCCCT GTCCCCTCAG CTCCAGACGT AGGGGAGGGG 150  
TTGCCACAGA CTCCCTGCTT GAAGCCTGCC CTTGCCTAAG ATGCTGGTAA 200  
TGGCCATGGT ACCCCCTTCC GGGCATCTAC TCTGGTTTTTC GGCCA 245

(2) INFORMATION FOR SEQ ID :760:

(i) SEQUENCE CHARACTERISTICS:  
20 (A) LENGTH: 68 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :760:

GCCAGCGCCG AGGTCGCATA TTTCTAGGCG CAGGTATATG ACTGCCATAT 50  
AACAAAAACC NTGAAAAC 68

(2) INFORMATION FOR SEQ ID :761:

35 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 71 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

380

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 64 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :757:

10

GCCTGCGCCG ACCACCCCTT CCTTTTTTTT ATCCAGCACA GCAAGACCAA

50

CAGGATTCTC TTCC

64

15

## (2) INFORMATION FOR SEQ ID :758:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 243 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

20

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID :758:

GCCAGCACCA AGTGACGCCA AAGCCCCTAG TTGACTCTAA CAGCCCCGTG

50

GGCGCGCGGG AGGCCGAGCG CTCTAGGGTC TACCTATCAG CGCAATCGTT

100

30

TAGCGCTTTT TCAATGGGGC AGGGCAGGAA GCAGGCGGGA CCAGGCAGCC

150

AGTTCTCAAA GGCTGCGGGG CCGACTAGAG GCCACAGCCC CTCACCCCTA

200

35

GACGTCGACA ACCAGAACTG ACGTGCGACC TCCCGGGCGC CGA

243

## (2) INFORMATION FOR SEQ ID :759:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 245 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

40

379

CCGGGCTGCG CCGAGCCATG GAACCATGGG AAGACCTTCA CTT

243

(2) INFORMATION FOR SEQ ID :755:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 71 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :755:

15 GCCAGCGCCG AGGTTGCATA TTTCTAGGCG CAGGCATATG ATTGCCATAT 50  
AACAAAAACC TGAAAGCATC A 71

(2) INFORMATION FOR SEQ ID :756:

20

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 243 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :756:

30

GCCACCGCCG AGTGACGCCA AAGCCCTTGG TTGACTCTAA CAGCCCCGTG 50  
GGCGCGCGGG AGGCCGGGCG CTCTAGGGTC TACCTATCAG CGCAATCGTT 100  
35 TAGTGCTTTT TCACTGGGGC GGGGCGGGAA GCAGGCGGGA CCAGGCAGCC 150  
AGTTCTCAAA GGCTGCGGGG CCGACTAGAG GCCACAGCCC CTCACCCCTA 200  
GACGTCGCCA ACCAGAACTG ACGCGCGACC TCCTGGGCGC TGA 243

40

(2) INFORMATION FOR SEQ ID :757:

378

GCCAGCACCG AGGTTGCATA TTTCTAGGCG CAGGCATATG ATTGCCATAT 50

AATAAAAAAA TGAAAACACC CC 72

5 (2) INFORMATION FOR SEQ ID :753:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 122 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :753:

GCCAGCGCCG AGGACACCAA GAAGGTTTTG GACAGCGTGG GCATCGAGGC 50

GGACAACAAC CAGCTCAACA AGGCCATTAG TGAGCTGAAT GAAAAAACA 100

20 TTGAAGACGT TATTGNCCAG GA 122

(2) INFORMATION FOR SEQ ID :754:

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 243 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :754:

35 GCCACCGCCG ACTGAAACTG CACCGACCCC CCCTCGAGGA CCTGCTCTTA 50

GGTTCAGAAG CAAACCTCAC GTGCACACTG ACCGACCTAA GAGACGCCTC 100

AGGCGCCACC TTCACCTGGA CACCCTCAAG CGGGAAGAGC ACTGTTCAAG 150

40 GACCACCTAA GCATGACCTC TACGGCTGCT ACAGCGTGTC CAGTGCCCTG 200

377

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :750:

GCCTACGCCG AAAACCCCTT CCTTTTTTTC ATCCAGAAAA GCAAGAGAAA 50

AAGGATTCTC TTCTGCGGCC GCCAACGCGT CGGAGAT 87

10

(2) INFORMATION FOR SEQ ID :751:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 170 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :751:

GCCTCCGCCG ATTCGTGACC AAGAAGGCTC TATGCATTCA GGCTTTCCAG 50

25 GAGACTCAAA AGCTGAAGAA GCAAAGAAGA GCCTTAAAGG CTGCAGCAGC 100

AGTCCNAAAA ACAAGCAGAG CAGAGGAACC CAGACAGCCC TGCCAAAGCC 150

ATGCCAAAGA CACTCAAAGA 170

30

(2) INFORMATION FOR SEQ ID :752:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 72 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :752:

376

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :748:

GCCAGCACCG ATGAATTCCC TTTGACCCAA GTCTGCAGCA GGTCCCTTTT 50  
GCGCTTCCTT CCCCTCAGGC AGCCTCTTTC CCCCTGGGCC ACTCCCGGGG 100  
10 GCGAGGGGGC TACCCCTTTC CCAGGCTTTT TATTCCCGTG GGGCTCACCC 150  
CAAAGCATTAA AAAGCAGCTT TGCAATTC 178

15 (2) INFORMATION FOR SEQ ID :749:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 235 base pairs  
(B) TYPE: nucleic acid  
20 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :749:

GCCAGCACCG AAAAGCCAAG ACTTCATGAA CTACACAGGT CTTACCATTG 50  
ACCTAAGATC AATCTGAACT ATCTTAGCCC AGTCAGGGAG CTCTATTCTT 100  
30 AGAAAGGCAT CTTTCGCCAG TGGATTCGCC CCAAGGTTGA GGCCGCCATT 150  
GGAAGACGAA AAATTGCACT CCCTTGGCGC AGACAAACAC CAGTTCCCAT 200  
35 TGGCGCTGCT GCCTATAACA AACACTTTTT TTTT 235

(2) INFORMATION FOR SEQ ID :750:

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 87 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double

375

GCCAGCTCCG AGGTTGTATA TTTCCAGGTG CAGATATATG ATTGCCATAT 50

AATAAAAATC TGAAAACATC CCAC 74

5 (2) INFORMATION FOR SEQ ID :746:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 88 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :746:

GCCTGCGCCG ACGATGCCCA GAATCCAGAA CTTTGTCTAT CACTCTCCCC 50

20 AACAAACCTAG ATGTGAAAAC AGGATAAACT TCACCCAG 88

(2) INFORMATION FOR SEQ ID :747:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 88 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :747:

GCCTGCGCCG ACGATGCCCA GAATCCAGAA CTTTGTCTAT CACTCTCCCC 50

35 AACAAACCTAG ATGTGAAAAC AGAATAAACT TCACCCAG 88

(2) INFORMATION FOR SEQ ID :748:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 178 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double

374

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 64 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :743:

10

GCCTGCGCCG ACCACCCCTT CCTTTTCTTG ATCTAGCACA GCAAGACCAA

50

CGGGATTCTC TTCT

64

15

## (2) INFORMATION FOR SEQ ID :744:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID :744:

GCCAGCGCCG AGGTTGTATA TTTCTAGGTG CAGGTATATG ATTGCCATAT

50

AATAAAAATT TGAAAACAT

69

30

## (2) INFORMATION FOR SEQ ID :745:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 74 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

40

## (xi) SEQUENCE DESCRIPTION: SEQ ID :745:

373

CCGGCATGTT CTTGTCACAC TGGGTGAGAA GATGACAGAG GAAGA

245

(2) INFORMATION FOR SEQ ID :741:

5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 88 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :741:

15

GCCTGCGCCG ACGATGCCCA GAATCCAGAA CTCGTCTAT CACTCTCCCC

50

AACAACTAG ATGTGAAAAC AGAATAAACT TCACCCAG

88

(2) INFORMATION FOR SEQ ID :742:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 242 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

25

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :742:

30

GCCGGAGCCA AAGCAAGCCA GAAGACTAAC AGTACTAACT ACAAATATTC

50

GCACCTCGAT CGCAGTACCC AGGTTCTCAC GTAGCTGAAG NAATGTATTA

100

35

CTCTGATAGT CTTCAATCGG ATAGACTAAA GCGTGTGCTG ACTGGAGATG

150

AGGTAAAGAA GATATGTATG CAACGTCCAG TCAAAACGGA TGGCAAGGTT

200

CGAGTCATGT CATATACCTT GCTGGATTAA TGGATGTCAT TA

242

40

(2) INFORMATION FOR SEQ ID :743:

## (xi) SEQUENCE DESCRIPTION: SEQ ID :738:

5 GCCAGCGCCG ACAATGCCCA GAATCCAGAA CTTGCCTAT CACTCTCCCC 50  
AACAACCTAG ACGCGAAAAC AGAATAAACT TCACCCAG 88

## (2) INFORMATION FOR SEQ ID :739:

10 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 95 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear  
15

## (xi) SEQUENCE DESCRIPTION: SEQ ID :739:

20 GCCAGCGCCG AGATCCTGGC GGCCTACCGC CCCCCGTGCA CCCCCGCTAG 50  
CGCCCCACCC CGCGTCTACC GCCCAATAAA GGCATCTTTG CCGGG 95

## (2) INFORMATION FOR SEQ ID :740:

25 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 245 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
30 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :740:

35 GCCACCCCGA AGACGTATCA AGGCCCTCGA ACAACCCCGA GAGCTGATGA 50  
GATGAATGAG AAGATGCCGA ACTTTGCGCA CTCCATGCCC CTGCTGCAGA 100  
40 CAGTAACCAA GAGCAAGGAC CAGGGCACCC ATGAGGATTA TGTCGAAGGA 150  
CTTCGGGTGT TTGACAAGGA AGGAAATGGC ACCGTCATGG GTGCTGAAAT 200

371

## (2) INFORMATION FOR SEQ ID :736:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :736:

GCCAGCGCCG ACCACAGGGC CTTGAATCCT TTTTGTTTT CAACAGTCTT 50  
GCTGAATTAA GCAGAAAGGG CCTTGAATCC TGGCCTAGAA TTTGGGCAGA 100  
TACAGCATTA ACAAACCGC GCATCTC 127

## (2) INFORMATION FOR SEQ ID :737:

20

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 64 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID :737:

30

GCCTGCGCCG ACCACCCCTT CCTTTTCTTC ATCCAGCACA GCAAGACCAA 50  
CAGGATTCTC TTCT 64

35

## (2) INFORMATION FOR SEQ ID :738:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

370

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :733:

GCCAGCGCCG AGATCCTGGC GGCCTACCGG CCCTCAGTGC ACCCCCGCTA 50

GCGCCCCACC CCGCGTCTAT CGCCCAATAA AGGCATCTTT GCCGGG 96

10

(2) INFORMATION FOR SEQ ID :734:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 96 base pairs

15

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :734:

GCCAGCGCCG AGATCCTGGC GGCCTACCAG CCCTCCGTGC ACCCCCGCTA 50

25

GCGCCCCACC CCGCGTCTAT CGCCCAATAA AGGCATCTTT GCCGGG 96

(2) INFORMATION FOR SEQ ID :735:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 97 base pairs

30

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :735:

GCCAGCGCCG AGATCCTGGC GGCCTACCAG CTCCTCAGTG CACCCCACT 50

40

AGCACCCAC CCCGCATCTA TCGCCCAATA AAGGCATCTT TGCCGGG 97

369

GCCTGCGCCG ACCACCCCTT CCTTTTCTTC ATCCAGCACA GCAAGACCAA 50

CAGGATTCTC TTCT 64

5 (2) INFORMATION FOR SEQ ID :731:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 96 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :731:

GCCAGCGCCG AGACCCTGGC GGCCTACCGG CCCCCCGTGC ACCCCCGCTA 50

20 GCGCCCCACC CCGCGTCTAT CGCCCAATAA AGGCATCTTT GCCGGG 96

(2) INFORMATION FOR SEQ ID :732:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 84 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :732:

GCCTGCGCCG ACCACCCCTT CCTTTTCTTC ATCCAGCACA GCAAGACCAA 50

35 CAGGATTCTC TTCTGCAGCC GCCACCGCGT CGGA 84

(2) INFORMATION FOR SEQ ID :733:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 96 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double

## (xi) SEQUENCE DESCRIPTION: SEQ ID :728:

5 GCCAGCGCCG AAAAGCCAAG ACTTCATGAA CTACACAGGT CTTACCATTG 50  
ACCTAAGATC AATCTAAACT ATCTTAGCCC AGTCAGGGAG CTCTATTCCT 100  
AGGAAGGCAT CTTTCGCCAG TGGATTGCC TCAAGGTCGA GGCCGCCACT 150  
10 GGAAGACGAA AAATAGAACT CCCTTAGAGT AGACAA 186

## (2) INFORMATION FOR SEQ ID :729:

## (i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 167 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID :729:

25 GCCAGCGCCG AGGTTGCATA TTCTAGGCGC AGGTATATGA TTGCCATATA 50  
ATAAAAACCT GAAAACATCC CACCCGGGAA AAAAAAAAAA AAAAAAAAAA 100  
AAAAACACCC CCCCCCACA AAAAATCAA ATTCCCCTCC CAAAAACCC 150  
30 CCTCAAAATC AAAAAAC 167

## (2) INFORMATION FOR SEQ ID :730:

## (i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 64 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

## (xi) SEQUENCE DESCRIPTION: SEQ ID :730:

367

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :726:

CCGTGTACTA TTAGCCATGG TCAACCCAC CGTGTTCTTC GACATTGCCG	50
TCGACGGGAG CCCTTGGCGC GCGTCTCCTT TGAGCTGTTT GCAGACAAGG	100
TCCCAAAGAC AGCAGAAAAT TTTCGTGCTC TGAGCACTGG AGAGAAAGGA	150
TTTGTTTATA AGG	163

(2) INFORMATION FOR SEQ ID :727:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 105 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :727:

GAGGGCGAGT TCGAGGAGGA GGCTGAGGAG GAGGTGGCCT AGAGCCTTCA	50
GTCAGTGGGG AAAGCAGGGA AGCAGTGTGA ACTCTTTATT CACTCCCAGC	100
CTGTT	105

35

(2) INFORMATION FOR SEQ ID :728:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 186 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

366

## (2) INFORMATION FOR SEQ ID :724:

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 164 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :724:

GTGTACTATT AGCCATGGTC AACCCACCG TGTTCTTCGA CATTGCCGTC 50  
15 GACGGGCGAG CCCTTGGCGC GCGTCCTTG AGCTGTTTGC AGACAAGGTC 100  
CCAAAGACAG CAGAAAAATT TTTCGTGCTC TGAGCACTGG AGAGAAAGGA 150  
TTTGTTTATA AGGG 164

20

## (2) INFORMATION FOR SEQ ID :725:

## (i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 110 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :725:

GTGAGAAGCT GCAGCGGTGA CCTGGAGGCT GCGATGTGGA GGTGGAGGAC 50  
35 ACACCCTCAA CCGTTGCTCC TGTAGCTTCC GAGTCCTGGT GGTGTCGGCC 100  
AAGTTCAGTA 110

40

## (2) INFORMATION FOR SEQ ID :726:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 163 base pairs

365

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :721:

GACCACCCCT TCCTTTTCTT CATCCAGCAC AGCAAGACCA ACGGGATTCT 50

CTTCT 55

10

(2) INFORMATION FOR SEQ ID :722:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 92 base pairs

15 (B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :722:

GACTTCACGA ACTACACAGG TCTTACCATT GACCTAAGAT CAATCTGAAC 50

25 ATTCTTAGCC CAGTCAGGGA GCTCTGCTTC CTAGAAAGGC AT 92

(2) INFORMATION FOR SEQ ID :723:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 55 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :723:

TATTTCTAGG TGCAGGTATA TGATTGCCAT ATAATAAAAA TCTGAAAACA 50

40

TCCCC 55

364

ACAAGGTCCC AAAGACAGCA GAA

123

(2) INFORMATION FOR SEQ ID :719:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 54 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :719:

15 ACCACCCCTT CCTTTTCTTC ATCCAGCACA GCAAGACCAA CGGGATTCTC 50  
TTCT 54

(2) INFORMATION FOR SEQ ID :720:

20

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 117 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :720:

30

GACCACAGGG CCTTCAATCC TTTTTTGTTC TCAACAGTCT TGCTGAATTA 50  
AGCAGAAAGG GCCTTGAATC CTGGCCTGGA ATTTGGGCAG ATATAGCATT 100  
35 AATAAAACTG TGCACTC 117

(2) INFORMATION FOR SEQ ID :721:

40

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 55 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double

363

(xi) SEQUENCE DESCRIPTION: SEQ ID :716:

GCCGAGGAGA ACCCCCGCTC CCTGAGGAGG ACCTGTCCAA ACTCTTCAAA 50  
5 CCACCACAGC CGCCTGCCAG GATGGACTCG CTGCTCATTG CAGGCCAGAT 100  
AA 102

(2) INFORMATION FOR SEQ ID :717:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 124 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :717:

20

AGCGAATGTA ACCCGGCCTT GGACGACCCG ACGCCGGACT ACATGAACCT 50  
GCTGGGCATG ATCTTCAGCA TGTGCGGCCT CATGCTTAAG CTGAAGTGGT 100  
25 GTGCTTGGGA TACGCTGTCT ACAG 124

(2) INFORMATION FOR SEQ ID :718:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 123 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :718:

GGAAAACCGT GTACTATTAG CCATGGTCAA CCCCACCGTG TTCTTCGACA 50  
40 TTGCCGTCGA CGGGAGCCCT TGGCGCGCGT CTCCTTTGAG CTGTTTGCAG 100

362

## (2) INFORMATION FOR SEQ ID :714:

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 90 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :714:

CTTGGGAGAT AACAGTTTCC CCTCTCCCTC CCCCTGCAGA TTCCAGCGC 50  
15 CCGGACCAAG GCCAAGTAAG CCTCTACAAA CCTAGCATTT 90

## (2) INFORMATION FOR SEQ ID :715:

## (i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 69 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID :715:

CCAGCGCCGA GGTGTATAT TTGTAGGTGC AGGCACACGA CCAGGACACA 50  
30 ACAAAAATCT GAAACATC 69

## (2) INFORMATION FOR SEQ ID :716:

35

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

361

(xi) SEQUENCE DESCRIPTION: SEQ ID :711:

CCAGCCAAAG ATTCCCAGGC TTTCTTGTCT CAGCAACTTT CCCATCTTCT 50  
5 CTCTCTTGGA TGATGTTTGC CGTCAGCATT CACCAAATAA ACTTGCTCTC 100  
TGGG 104

(2) INFORMATION FOR SEQ ID :712:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :712:

20

CTAGAAATAG ACCCACAATT TAGAGACAAT CTATACTAGA TTTATCTCCT 50  
TTGTTTTTAG TTGAAGGC 68

25

(2) INFORMATION FOR SEQ ID :713:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 base pairs
- (B) TYPE: nucleic acid
- 30 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :713:

AGCGAATGTA AGGGGGCCTT GGACGACCCG ACGCCGGA CTATGAACCT 50  
GCTGGGCATG ATCTTCAGCA TGTGCGGCCT CATGCTTAAG CTGAAGTGGT 100  
40 GTGCTTGGGT CGCTGTCTAC TGCTCCT 127

360

## (2) INFORMATION FOR SEQ ID :709:

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 51 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :709:

GCCAGCACCG AGCAACCTGG GTCCAAATAA AAATAAACT GCAAATCCT 50

15 G 51

## (2) INFORMATION FOR SEQ ID :710:

## (i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 64 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID :710:

GCCTGCGCCG ACCACCCCTT CCTTTTCTTC ATCCAGCACA GCAAGACCAA 50

30 CAGGATTCTC TTCT 64

## (2) INFORMATION FOR SEQ ID :711:

35

## (i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 104 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

359

TCAGGGAGT

209

## (2) INFORMATION FOR SEQ ID :707:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 170 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :707:

15 GCCAGCACCG AGATGACGAG CTTTCTGCTG CCACCCACAA GCAGAGGGAC 50  
TCGGAGATCA CGCAGCAGAA GCAGAAAAAG GCAAACAAGA AGAAGGAGGA 100  
ACCCAAGCAG CTTTGCGGCT TCACGCCCAA CCCTCTCGCC CTTACCTGT 150  
20 GAGCCTGGAG CCAGTCCCAC 170

## (2) INFORMATION FOR SEQ ID :708:

- 25 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 160 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :708:

35 GCCACCGTCG AGGATTCAGC AGCCTCCCCC TTGAGCCCCC TCACTTCCCG 50  
ACGTTCCGTT TCCCCCTGCC CGCCTTTTTC CGCCACCACC GCCGCCGCCT 100  
TCTGCAGGCC GTTTCACCG AGGAAAAGGA ATCGTATTGT ATACCCGCTA 150  
40 CCCAGAACCT 160

358

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 262 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :705:

10

GCTTGATGCC TGCGCCGAAC AAACATACAG AATGCGGCGA GTCCCTCTGG 50  
ACGCCCAACA CGGATCCGGA TCACCTATCT GAAACCATCT CCCAAGCCAT 100  
GCTGAATGCT GCGGACCAGG ATGCAGTGCC AGGCATGGGA GCCATTGCCC 150  
ACATCACC GAAGGACAAA ATCACCACCA GGACACTGAA GGCCCGAATG 200  
GACTAACCT GTTCCCAGAG CCCACTTTTT TTCTTTTCA GAAATAAAAC 250  
AGCCTGTCTT TC 262

20

## (2) INFORMATION FOR SEQ ID :706:

25

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 209 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :706:

35

GCCAGCACCG ACCTAGCCTA AGCCGTCTAA AACCACCTGA GCCCCTGAGG 50  
AAACCTGTGG TCACACTGGG CCCTCCTCAG GAACTCTCCC TGCGCAGAGG 100  
CGTGTCTTAG CACTGCCCCC CTCCCTAGCC CCTTATTTGG CGGCGGAAGC 150  
GGCCTCCACC CCTTCCCTGT TTGCAAACAC TCTGCGGAGA AAAGAGGACT 200

40

357

(xi) SEQUENCE DESCRIPTION: SEQ ID :702:

5 GCCTGCGCCG AGCACAAGAC AATGATGAAC ATTCTAAAAA AAAAGAATGA 50  
CGCACATTTT AATAAAGCAC AGCACAAACT GTTCTTTCC 89

(2) INFORMATION FOR SEQ ID :703:

10 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 96 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :703:

20 GCCAGCGCCG AGATCCTGGC GGCCTACCGC CCCCCGCCGC ACCCCCGCTA 50  
GCGCCCCACC CCGCGTCTAT CGCCCAATAA AGGCATCTTT GTCGGG 96

(2) INFORMATION FOR SEQ ID :704:

25 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 123 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :704:

35 GCCTGCGCCG AACAAACATA CAGAACGCAA CGAGTCCCTC TGAAGGCCCA 50  
ACACGGATCC GAATCACCTG GCGCGAAACC ACCTACCTAG CCATGATGAA 100  
40 TGCTGAGGAC CCAGATGCAG TAC 123

(2) INFORMATION FOR SEQ ID :705:

356

GGAGGCTCAA AAGAGGACAC AAAAGTGAAC AGAATGATCT TCCTACGCAC 100  
AACACAAACA TCAGTTAATG CTCCATCCAC GCTGCTTAAA GAGCATTCCT 150  
5 GTCCTAGCAA AATGGGCAAG TCCCTCTACC CCCCACCCTC ACTTGGCATG 200  
CTTACATTAA TAGCTAAAGT CAATCCTGTA ATGAAATAAA GCAAATGGCA 250  
GCTGTCTAGT AGCCTCCACT ACCGCAAATA TC 282

10

(2) INFORMATION FOR SEQ ID :701:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 255 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :701:

GCCTGCGCCG AACAAACGCA CGGAATGAGC GAGTCCCTCT GGGAGCCCCAA 50  
25 CATGGATCCG AATCACCTGT TTGAAACCAT CTCCAAGCC ATGCTGAATG 100  
CTGCGGACCA GGATGCAGTG CCAGGCATGG GAGTCATTGC CCACATCACC 150  
GAGAAGGACA AAATCACCAC CAGGACACTG AAGGCCCGAA TGGACTAACC 200  
30 CTGTTCCCAG AGCCCACTTT TCCCCTATTT TGGAAATAAA ATAGCCTGTC 250  
TTTCG 255

35

(2) INFORMATION FOR SEQ ID :702:

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 89 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

355

GGCTTCTGTG AGCACCGTGC TGACCTCCAA ACACCGTTAA GCTGGAGCCT 100  
CGGTAGCCGT TCCTCCTGCC CACTGGACTC CCAACAGGCC CTCCTCCCCT 150  
5 CCTTGCACCG GCCCTTCCTG GTCTTTGAAT AAAGTCTAAG CGGGCAGC 198

(2) INFORMATION FOR SEQ ID :699:

(i) SEQUENCE CHARACTERISTICS:  
10 (A) LENGTH: 230 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :699:

GCCAGCACCG ACAGCAACAA AAATGTTCCC ACAGAGATCA GGATGACTTG 50  
20 CTGAAGCTCA GTGGAGGCTA AAAAGAGGAC ACAAAGTGA ACAGAATGAC 100  
CTTCCTACGC ACAACACAAA CACCACTTAA TGCTCCATCC ACGCTGCTTA 150  
25 AAGAGCATTC CTGTCCTAGC AAAATGGGCA AGTCCCTCTA CCCCCACCC 200  
TTAGCCGGCA TGCTTACATT AATAGCTAGA 230

(2) INFORMATION FOR SEQ ID :700:

30

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 282 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
35 (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :700:

AGCAACAAAA ATGTTTCCAC GGAGATCAGG ATGACTTGCT GAAGCTCAGT 50

354

CCAACAACAC AGACGGCGAA AACAAAACAA ACTTAAACCT AG

92

## (2) INFORMATION FOR SEQ ID :697:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 314 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :697:

15 GCCAGCACCG AGGCCTAGGG TAGAGCAGAC TGTGGCTTTA CCTCGGTGTC 50  
CTACCAGCAA GGGGTCCTAT CTACCACCAT CCTCTATGAG ATCCTGCTAG 100  
GGAAGGCCAC CCTGCATGCT GCGTTGGTCA GCACCCTTGC GCTGATGGCC 150  
20 ATAGTCAAGA GAAAGGATTT CTGAAGGCAG CCCTAGAAGC GGAGTTAGGA 200  
GCTTCTAACC CGTCATGGTT TAAATACACA CCCTTTTTTG GACAGCGCTT 250  
CTGAAGAGCT GCTCTTACCT CTCTGCATCC CAATAGATAT CCCCCTATGC 300  
GCATGCGTAC CTGT 314

## (2) INFORMATION FOR SEQ ID :698:

30

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 198 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
35 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :698:

40

GCCACGCGCG AGTTCACCCC TGCAGTGCAC GCCTCCCTGG ACAAGTTCCT 50

353

GGATGCAGTG TCAGGCATGG GAGTCATTGC CCACATCATC GAGAAGGACA 200

AAATCACCAC CAGGACACTG AAGGCCCGAA TGGACTAACC CTGTTCCCAG 250

5 AGCCCACTTT TTTTTTTTTT TTGGAAATAA AATAGCCTAT CTTTCG 296

(2) INFORMATION FOR SEQ ID :695:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 211 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :695:

GCCAGCACCG ACCTAGCCTA AGCCGTCTAG AACCACCTAA GCCCCTAAGG 50

20 AAACCTGTGG TCACACTGGG CCCTCCTCAG GAACTCTCCC TGC GCAGAGG 100

CGTGTCTTAG CACTAACCTC CTCCCTAGCC CTTATTTGG TGGCAGAAGT 150

25 GGCCTCCACC CCTTCACCGT TTAAAAATAC TCCGTGGAGA AAAGAAAGCT 200

TNAAGGAGTA G 211

(2) INFORMATION FOR SEQ ID :696:

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 92 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
35 (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :696:

GCCTGCACCG ACAATGCCCA GAACTCCAGA ACTTCACCTA TCACGTATCC 50

352

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 329 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :693:

10

TCTGCTGCCG CCCGCAAGCA GAGGGACTCG GAGATCATGC AGGGGAAGCA 50  
GAAAAAGGCA AACAAGAAGA AGGAGGAACC CAAGCAGCTT TGCGGCTTCG 100  
CGTCCAACCC TCTTGCCCTT CACCTACGCG CCTAGAGCCA GTCCCACCAC 150  
GCTCGCGTTT CCTCCTGTAG CGCTCACAGG CCCCAGCACC GATGGCATTC 200  
CCTTTGACCT AAGCCTACAG CAGGCCCCTT TTGTGCTTCC TTCCCCTCAG 250  
GCAGCCTCTT TCCCCCTGGG CCACTCCCGG GGGTGAGGGG GTTGTCTTC 300  
CCGATGCTTT TTGTTACCGT GGGGTTTGC 329

20

25

## (2) INFORMATION FOR SEQ ID :694:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 296 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

35

## (xi) SEQUENCE DESCRIPTION: SEQ ID :694:

TCTGCTGCCG CCCGCAAGCA GAGGGACTCG GAGATCATGC CCTGCGCCGA 50  
ACAAATGTAC GGAATGCGTG AGTCCCTCTG GGAGGCC CACGGATCCG 100  
GATCACCTGT TTGAAACCAT CTCCAAGCC ATGCTGAATG CTGCGGACCA 150

40

351

ACACAAATTC ACAAGTGNTC TCAAAAACT C

81

(2) INFORMATION FOR SEQ ID :691:

5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 217 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :691:

15

TTCCTAACCG ATCGAATGAA GGATTCAAAA TTAACCACTC CAAGGGGGGA

50

TTGAAGGAAG AACCACTCTT AACGGACAAA AAGAAAGAAA GGGGAGGGAG

100

TAACAGGGAT ATGAGCTCTA GCCGCCCAAG CTAGCAATGG CAACCCTTCT

150

20

GGGTCCCCTT TCAGCATGCG GAAGCTTTTC TCGACTTCA CTCCATAAAC

200

AGCTGACGCT CAAAAAG

217

25

(2) INFORMATION FOR SEQ ID :692:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 72 base pairs

(B) TYPE: nucleic acid

30

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :692:

CGGCCTTCTG GAAACCCATG AAAAAAAAAA GTTCCGCACC TCCAAGGGGA

50

GAAGAGTAAG AGACAGCTTT CA

72

40

(2) INFORMATION FOR SEQ ID :693:

350

GCCTCTCTCT GGGCAAGTTC ATGGCTTCTG TGAGCCCTTT NACTGACCTC 50  
CAGACACTGT TAGGCTGGAG CCTCGGTAGC CGTTCCTCCT GCCCACTGGA 100  
5 CCTTCCAACA GGCCCTCCTC CCCTCCTTGA ACCGGCCCTT CCTGGCCTTT 150  
GAATAGAGTC TAAGCGAACG AC 172

## (2) INFORMATION FOR SEQ ID :689:

10

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 200 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 15 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :689:

20

GCCACCGCCG AGCTCACCCC TGCGGTGCAC GCCTTCCTTG GACAAGTTTT 50  
TGGCTTCTGC GAGCCTTTTA CTGACCTCCA AACGCTGTTA AGCCGGAGCC 100  
25 TCGGTAGCCG TTCCTCCTGC CCACTGGACN TCCCAACGGG CCCTCCTCCC 150  
CTCCTTGAAC CAGCCCTTCC TGGCCTTTGA ATAAAGTTTA AGCGAGTAGC 200

## (2) INFORMATION FOR SEQ ID :690:

30

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 81 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 35 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :690:

40

GCCACCGCCG AGCAGCAGCT TACAGCCAGG GCAGCTTTGA ATGCGGCCCA 50

349

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :686:

ACATGCCAAA GAAAGCGTGC ATATTAGCCT ATAGAACCAC AGTAATCACA	50
CTAGAGAAAT TCCACTGCTA CAATAAAATG TAATCGGAAG CATCTTTACT	100
TATAAA	106

15

(2) INFORMATION FOR SEQ ID :687:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :687:

CAGATTTTTT TCAATTCTCC ACCCGCCAAA AGGGGAAGGG CTTTCCCCCA	50
GAGAAAAGGA AAGGGGGGAA AAGGGGAAAA AACCCAACCC AAAACCA	97

30

(2) INFORMATION FOR SEQ ID :688:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 172 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :688:

## (xi) SEQUENCE DESCRIPTION: SEQ ID :684:

5 AGCACCGAGG CGCTCAAGGT CCTGGGGAAC CCCAAGAGCG ACGAGACGAA 50  
CGCGAAGGCG CTGGACTTTG AGCACTTTCT GCCCATGCTG CAGACAGTGG 100  
CCAAGAACAA GGACCAGGGC ACCTATGAGG ATTATGCCGA AGGACTTCGG 150  
10 GCGCTTGACA AGGAAGGAAA TGGCACCGTC ATGGGCGCTG AAACCCGGCA 200  
TGCTCTTGCC AACTGGGCG AGAAGACGAC AGAGGAAGAA GCAGAGACGC 250  
TGGCGGCAGG GCATGAGGAC AGCAATGGTT GCATCAACTA CGAAGCATTT 300  
15 GTGAGGC 307

## (2) INFORMATION FOR SEQ ID :685:

20 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 174 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear  
25

## (xi) SEQUENCE DESCRIPTION: SEQ ID :685:

30 CCATCTCAAG GCGATCCATG GAAAGCTTCC TGGGGAACGT ATGCTAGCAG 50  
AGCTTCTCCC CGTGAATCAC ATGCCGAGA TCCCACTCTT AGCTGGCAAA 100  
TGAATCCGAA TTGACACAGC AGCCCCATAA GCATCAGCCC TGTAGAGTGA 150  
35 GGAGCCATCT CTAGCGGGCC CTTC 174

## (2) INFORMATION FOR SEQ ID :686:

40 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 106 base pairs  
(B) TYPE: nucleic acid

347

	GCCACCGCCG AGGAAAACCG TGCACTGTTA GCCATGATCA ACCCCACCGT	50
	GCTCTTCGAC ATTGACATCG ACGGCTGAGC CCTTGACCTA GTCTCCTTTG	100
5	AGCTGTTTGC AGACAAGGTC CCAAAGACAG CAGAAAATTT TCGTGCTCTA	150
	AGCACTGGAG AGAAAGGATT TGTTTATAAG GGTTCCTGCT TTCACAGAAT	200
	TATTCCAGGG TTTATGCGCC AGGGTGGTGA CTTCACACGC CATAATGGCA	250
10	CTGGTGGCAA GTCCATCCAT GGGGAGAAAT TTGAAGACGA GAACTTCATC	300
	CTAAAGCATA CGGGCCCTGG CATCTTGCCC ATGGCAAATG CTGATCCTGA	350
15	TACA	354

## (2) INFORMATION FOR SEQ ID :683:

## (i) SEQUENCE CHARACTERISTICS:

- |    |                            |
|----|----------------------------|
| 20 | (A) LENGTH: 148 base pairs |
|    | (B) TYPE: nucleic acid     |
|    | (C) STRANDEDNESS: double   |
|    | (D) TOPOLOGY: linear       |

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID :683:

30	CCTCTCCGTG AGGACAGGGC AGTCTTGGTG CGCAGCCCCT CTCCTCTCTG	50
	TCCCCTGACA CTCCACAGTG CGCCTGCAAC CCAGGCGGCC TTATCCGCGC	100
	AGTGGCGGCA GTTCAGAAAT AAAGGGCCCA TTTGCGGGAT GCCGCATT	148

## 35 (2) INFORMATION FOR SEQ ID :684:

## (i) SEQUENCE CHARACTERISTICS:

- |    |                            |
|----|----------------------------|
| 40 | (A) LENGTH: 307 base pairs |
|    | (B) TYPE: nucleic acid     |
|    | (C) STRANDEDNESS: double   |
|    | (D) TOPOLOGY: linear       |

346

CAGCCTGGGA TCCGGTGACG GCCTAGGCAG AGGCTGGGCC AGGAGTCCCA 200

AAGGTCAGTG ACAGTTTCTC AGAAGGGGCC CAGCGTCCAC CTCTCTCCCA 250

5 GGACCAGACA CCCCTTCCAG GCTCCCCCAC CCCCTACGG GCTC 294

(2) INFORMATION FOR SEQ ID :681:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 268 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :681:

CCGCCAAGTG ACACCAAAGC CCTGGTTGAC TTTGACAGCC CCGTGGGCGC 50

20

GCGGGAGGCC GGGCACTCTA GGGTCTACCT ACCAGTGCAA TCGTTTAGCG 100

CTTTTTCACT GGGGCAGGGC AGGAAGCAGG CGGGACCAGG CAGCCAGTTC 150

25

TCAAAGGCTG CGGGGCCAAC TAGAGGCCAC AGCCCCTCAC CCCTAGACAC 200

TGCCAACCAG AACTGACACG CGACCTCCTG GCGCTGACG CCATTAAAAC 250

CAACGTTGGC GCCCGGCG 268

30

(2) INFORMATION FOR SEQ ID :682:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 354 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :682:

345

## (2) INFORMATION FOR SEQ ID :679:

## (i) SEQUENCE CHARACTERISTICS:

5

- (A) LENGTH: 253 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :679:

GCCTGCCCCG ACACGAAGAT GACCCTCGAC AGCCGCCGGG CGCTGATCAC	50
CAGGGAAGGC AAAGGCATAG GCCAGCACCG ATGAATTCCC TTTGACCTAA	100
GTCTGCAGCA GGCCCCTTTT GCGCTTCCTT CCCCTCAGGC AGCCTCTCTC	150
CCCCCGGGCC ACTCCCGGGG GCGAGGGGGT TACCCCTTTC CCAGTGCTTT	200
TTATCCCCGC GGGGCTCACC CCAAAGCATT AAAAGCAGCT TTGCAATTCC	250
TTG	253

25

## (2) INFORMATION FOR SEQ ID :680:

## (i) SEQUENCE CHARACTERISTICS:

30

- (A) LENGTH: 294 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

## (xi) SEQUENCE DESCRIPTION: SEQ ID :680:

GCCAGCGCCG AGGCTTCTCC TAGGGCTGCT CCTGGGCCTA GCTCTTACAG	50
GCTCGTCCCC CAGGCCTGCC CTTCTCCACT GCCCCCTCCC GTGCCTGGGC	100
CCACACACCC TTCAGGAAGG GGGAGCACTG AGAAGCACAG CACAGGGGCT	150

344

ACCAGGGAAG GCAAAGGCAT AGGACTTCCA CACAGTCCAG AACTGCACG 100  
CTGACAAGCG CCTCCGCGGC GGCTGCGAGC CGGACTCAGG CGGATCTTGA 150  
5 CAGCCTTGCC CGCGAGTGCC CGGGGATAGA ACCCGTGCGC GTGGACCTAG 200  
GTGACTGGGA GGCCACCAAG CAGGCACTGG GCAGCGTGGG CCCCCTGGAC 250  
CTGCTGGAGA ACAACACCAC CGTCGCCCTG CCGCAGCCCT TCCAGGAGGT 300  
10 CACCAAGGAG GCCTTCGACA GATCCTTTGA GGTGAGCTTG CGTGCGATCA 350  
TCCAGGTGCT GTAGA 365

15 (2) INFORMATION FOR SEQ ID :678:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 366 base pairs  
(B) TYPE: nucleic acid  
20 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :678:

GCCTGCCCCG ACACGAAGAT GACCCTCGAC AGCCGCCGGG CGCTGATCAC 50  
CAGGGAAGGC AAAGGCATAG GACTTCTGCA CGGTCCAGAC CCATGTACGC 100  
30 GACGGGCGCC TNCGCGGTGG CTGCGAGCCG GATTCAGGCA GATCTTGACA 150  
GCCTTGCCCCG CGAGTGCCCCG GGGATAGAAC CCGTGTGCGT GGACCTNGGG 200  
TGACTGGGAG GCCACCAAGC AGGCACTGGG GTAGCATGGG CCCC GCGGAC 250  
CTGCCGGAGA ACAATACCAC CGCCGCCTNT GCCGCAGTCT TTCCCGGAGG 300  
TCACCAAGGA GGCCTNTTGA TAGATCTTTT GAGGTGAGCT TGC GTGCGGT 350  
40 CATCTAGGTG CTGTAG 366

343

(xi) SEQUENCE DESCRIPTION: SEQ ID :675:

5 GCCAGCGCCG ACACCCAGAG ACTACAGTAC TTAGGGGTTA CACACAACAG 50  
CCGTAAGTGG CGGCTATCTG TTCATAACAA ACAAACCATA GCATATTTAC 100  
ACCGCATCAC ATCGAGTGAT TATAGAAATC CATAACACA CCGATTGCAT 150  
AAAATCTTTT TTTAGGAAAA AAACAC 176

(2) INFORMATION FOR SEQ ID :676:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 141 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :676:

20 GCCAGCGCCG ACGCCCAGAG AATACAGTAC TTAGGGGTTA CACACAACAG 50  
25 CCGTAAGTGG CGGCTATCTG CTCATAACAA ACAAACCACA GCATATCTAT 100  
ACCGTATCAC ATCGAGTGAT TATAGAAATC CACAGAGAGA C 141

(2) INFORMATION FOR SEQ ID :677:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 365 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :677:

40 CTCTGAACAG ACACGAAGCT GCCCCTCGTA CAGCCACTCG GCGCTGACC 50

342

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :673:

	GCCTGCGCCG	ANGCATTCCC	TTTGACCTGA	GTCTGCAGCA	GGTCCCTTTT	50
10	GCGCTTCCTT	CCCCTCAGGT	AGCCTCTCTC	CCCCTGGGCC	ACTCCCGGGG	100
	GTGAGGGGGT	TACCCCTTCC	CAGTGTTTTT	TATTTCCGTG	GGGCTCACCC	150
15	CAAAGTATTA	AAAGCAACTT	TGCAATT			177

(2) INFORMATION FOR SEQ ID :674:

20	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 77 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear
25	

(xi) SEQUENCE DESCRIPTION: SEQ ID :674:

30	GCCTGCGCCG	AGCACAAAGAC	AATGACGAAC	ATTTTAAAAA	AAAAGAATGA	50
	CGCACATTTT	AATAAAGCAC	AGCACAA			77

(2) INFORMATION FOR SEQ ID :675:

35	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 176 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
40	(D) TOPOLOGY: linear

341

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :670:

GCCAGCGCCG AAAACACACA CTTTGCTTCT TACCTGC

37

(2) INFORMATION FOR SEQ ID :671:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 37 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

15

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :671:

20

GCCAGCGCCG AAAACACACA CTCTGCTTCT TACCTGC

37

(2) INFORMATION FOR SEQ ID :672:

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 59 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

30

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :672:

35

GCCACCGCCG ACTCCAGGCA CTCACTCAA CTCGATCTTC AACTCTGCAT

50

ACAAGCAGA

59

(2) INFORMATION FOR SEQ ID :673:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 177 base pairs

340

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :668:

10

GCCACCGCCG ACTCCAGGCA CTCACTCAA CTTGATCTTC AACTCTGCAT 50  
ACAAGCAGA 59

15

## (2) INFORMATION FOR SEQ ID :669:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 223 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID :669:

GCCTGCGCCG AACAAATATA CAGAATGCGC GAGTCCCTCT GGAAGCCCAA 50  
CATGGATCCG GATCACCTGT TTGAAACCAT CTCCAAGCC ATGCTGAATG 100  
CTGCGGACCA GGATGCAGTG CCAGGCATGG GAGTCATTGC CCACATCACC 150  
GAGAAGGACA AAATCACCAC CAGGACACTG AAGGCCCGAA TGGACTCGCC 200  
CTGCTCCCAG AGCCCACTTT TTT 223

35

## (2) INFORMATION FOR SEQ ID :670:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double

40

## (xi) SEQUENCE DESCRIPTION: SEQ ID :665:

5 GCCAGCGCCG AGGTTGCATA TTTCTAGGCG CAGGTATATG ATTGCCATAT 50  
AATAAAAATC TGAAAACACC 70

## (2) INFORMATION FOR SEQ ID :666:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :666:

20 GCCAGCGCCG ACCGCCCAA AAATACTCCC ACCGGGATCA GGGCGATTAA 50  
TGAAGACTCA ACGGGGACTA AAAAGGGGCC CCAAAAAAAAA CCAAACCACC 100  
TTTCTACGTA CCGTATAG 118

## (2) INFORMATION FOR SEQ ID :667:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :667:

GCCAGCGCCG ACGATGCCCA GAATCCAGGA CTTTGCCTAT CACTCTCCCC 50  
40 AACAACTAG ACGCGAAAAC AGAATAAACT TCACCCAG 88

## (2) INFORMATION FOR SEQ ID :668:

338

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :663:

GCCTGCGCCG ACGATGACCA GAATCCAGAA CTTTGCCTAT CACTCTCCCC 50  
10 AACAACTAG ACGCGAAAAC AGAATAAACT TCACCCAG 88

(2) INFORMATION FOR SEQ ID :664:

- 15 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 223 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :664:

25 GCCTGCGCCG ACAAACAAA CCTGGAGGCC ATTCTGCACA GCCTGCCCCGA 50  
GAACTGTGCC AGCTGGCGGT GAGGGCTGCC CAGATCCCCG GCACACACTC 100  
CCCCACCTGC TGTTTACATG ACCCAGGGGG CGCACACTAC CCCACAGGCG 150  
30 CGCCCATACA GACATTCCCC GGAGCCGGCT GCTGCGAACT CGACCCCGTG 200  
CGGATAGTCA CACTCCCTGC CGA 223

35 (2) INFORMATION FOR SEQ ID :665:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 70 base pairs  
(B) TYPE: nucleic acid  
40 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

337

## (2) INFORMATION FOR SEQ ID :661:

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 245 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :661:

AGGCACTGAC CCCTGCCACC CCTCACTGCA TTAAGTTCAG CCACGTCTCC 50  
15 TCCTTCCTCT GCGCTTCCAG TGATAAGGGT ACTGTCCATA TCTTTGCTCT 100  
CAAGGATACC CGCCTCAACC GCCGCTCCGG CCTGGCTCGC GTGGGCAAGG 150  
TGGGGCCTAT GATTGGGCAG TACGTGGACT CTCAGTGGAG CCTGGCGAGC 200  
20 TTCCTGTGC CTGCTGAGTC AGCTTGCATC TGCGCCTTCG GTGCG 245

## (2) INFORMATION FOR SEQ ID :662:

25

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :662:

35 GCCAGCGCCG AGGTCGCATA TTTCTAGGCG CAGGTATATG ATTGCCATAT 50  
AATAAAAACM TGAAAACACC CC 72

## (2) INFORMATION FOR SEQ ID :663:

40

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 base pairs

336

(xi) SEQUENCE DESCRIPTION: SEQ ID :658:

CCGACCACCC CTCCTTTTC TTCATCCAGC ACAGCAAGAC CAACGGGATT 50  
5 CTCTTCTGCG GCCGCCACCG CGTGGA 76

(2) INFORMATION FOR SEQ ID :659:

(i) SEQUENCE CHARACTERISTICS:  
10 (A) LENGTH: 68 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :659:

GCCAGCGCCG AGGTCGCATA TTTCTAGGCG CAGGTATATG ACTGCCATAT 50  
20 AACAAAAACC NTGAAAAC 68

(2) INFORMATION FOR SEQ ID :660:

(i) SEQUENCE CHARACTERISTICS:  
25 (A) LENGTH: 151 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :660:

35 CCCAACTTC TTAAAAATC AAGTAATGTT TACAAGAAAG AATAAAATCT 50  
TAATCCTTTT CACTTTTAAA GACAATCAGA TAAGATTACC CACTGCGATT 100  
AAACACTGAT CAAACTCAGT TGCCTTACG TTAGCATTAC TCTGTCATAG 150  
40 C 151

335

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :656:

10 CCACCCCTTC CTTTCTTCA TCCAGCACAG CAAGACCAAC GGGATTCTCT 50

TCTGCGGCCG CCACCGCGTG GA 72

(2) INFORMATION FOR SEQ ID :657:

15

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 178 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :657:

25 AGAGGGTTTT CTATATGTAA TTCTTTTATT CTGTAAAAGG TAACAAAATA 50

TACAGAACAA AAAAATTTC CCTTTTAAA ACTAATGTTA CAAATCTGTA 100

30 TTATCACTTG TATATAAATA GTATATAGCT GATCATTAAT AAGGTGTATA 150

GTACAATGTA TTCTAAAACT GTCCGCC 178

(2) INFORMATION FOR SEQ ID :658:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 76 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

334

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :654:

CCGCCTCAGA CTCTGGACCA GCCACTGTCC CAGAAGCCAG GCCGGGCAGT 50  
10 GGCCTTCTCC ACTCCCCTCT GACTTCTCCA AGGGGCTCAG TGGCCAGTGC 100  
CCCCCAGGAG GCTCCACCCT CAACTCAACC CAAGCAAGAG GGACAGATGA 150  
15 AAAACAAAAT CCAATCAGGG CGATAAATGG CGGGGGGTTT AATTTGGTTT 200  
CTGAGCGCAT AAAGCTAAGG AGGGGT 226

(2) INFORMATION FOR SEQ ID :655:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 167 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
25 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :655:

30

TTAAAAAAT TCCCCCTTT AATTGACCAA AGTAAAGCCA TGACATTTCA 50  
TTTGTAACC TGTTTAGAAT TATAAAATC ATTCATTTG GCCCAGCCCA 100  
35 TACGCCCAAG AGAAACTTC CAGACTTTTC TGATGCCATC CAGTTTTGTT 150  
CTTACAAAAT GCATATT 167

(2) INFORMATION FOR SEQ ID :656:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 72 base pairs

333

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :652:

10	CCGACAGACG GTCATTGATT ACAACGGGGA ACGCACGCTG GATGGTTTTA	50
	AGAAATTCCT GGAGAGCGGT GGCCAGGATG GGGCAGGGGA TGATGACGAT	100
	CTCGAGGACC TGGAAGAAGC AGAGGAGCCA GACATGGAGG AAGACNATGA	150
15	TCAGAAAGCT GTGAAAGATG AACTGTAATA CGCAAAGCCA GACCCGGG	198

## (2) INFORMATION FOR SEQ ID :653:

## (i) SEQUENCE CHARACTERISTICS:

20	(A) LENGTH: 224 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID :653:

30	CCGAAAAGCC AAGACTTCAT GAACTACATA GGTCTTACCA TTGACCTAAG	50
	ATCAATCTGA ACTATCTTAG CCCAGTCAGG GAGCTCTGCT TCCTAGAAAG	100
	GCATCTTTTCG CCAGTGGATT CGCCTCAAGG TTGAGGCCGC CATTGGAAGA	150
35	TGAAAAATTG CACTCCCTTG GTGTAGACAA TACCAGTTCC ATTGGTGTTG	200
	TTGCTATAAT AACACTTTTC TTTT	224

## (2) INFORMATION FOR SEQ ID :654:

40

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 226 base pairs

332

GGATTCTCTT CTGCGGCCGC CACCGCGTGG A

81

(2) INFORMATION FOR SEQ ID :650:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 159 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :650:

15 AGGAGCNCCG ACAAAGACA CATTGGACCT GTCAGCTCCT CTGTTTCACC 50  
AAGCAGACAC AATAACCTTA CCAACAAAGC AGAGTAAGCC AAGTGCCTCT 100  
GTGTGACACC ACCGCATNNT GATGACGCAT AATAAAAATA TAACTAATTT 150  
20 AGACTAGAG 159

(2) INFORMATION FOR SEQ ID :651:

- 25 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 78 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :651:

35 CCGACCACCC CTCCTTTTC TTCATCCAGC ACAGCAAGAC CAACGGGATT 50  
CTCTTCTGCG GCCGCCACCG CTGGAGCT 78

(2) INFORMATION FOR SEQ ID :652:

40

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 198 base pairs

331

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :647:

CAAGACAATA GTCACATCAT CGCAGCCTTG TTCTTTCCGA AGGATAAAAT 50

GTCATTCAAG AATGGGGTGA GGTGGTTAGA GGGAGTAGGT ACT 93

10

(2) INFORMATION FOR SEQ ID :648:

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 114 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :648:

CCCCTTTTGG TCCCCACTGA GATGTATGAA GGTTTGGTC TCCCTGGGAG 50

25 TGGGTGGAGG CAGCCAGGGC TTACCTGTAC ACTGACTTGA GACCAGTTGA 100

AAAGTGCACA CCTT 114

30

(2) INFORMATION FOR SEQ ID :649:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 81 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

35

(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :649:

CTGCNCCGAC CACCCCTTCC TTTTCTTCAT CCAGCACAGC AAGACCAACG 50

330

## (2) INFORMATION FOR SEQ ID :645:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 182 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :645:

CCACCACCCG ATTCGTGACC AAGAAGGCTC TGTGCATTCG GGTTTTCCAG 50  
GAGACTCAAA AGCCGAAGAA GCGAAGAAGA GCCTTAAAGG CTGCAGCAGC 100  
CAGAAAAACA AGCAAAGGAG GAACCCAGAC AGCCCTGCAA AGCATACAAG 150  
ACACTCAAGA CAGCAATTAA TCTGTCATCA TT 182

20

## (2) INFORMATION FOR SEQ ID :646:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :646:

CCAGCGCCGA GGTTGTATAT TTCTAGGTGC AGGTATATGA TTGCCATATA 50  
ATAAAAATCT GAAAAC 66

35

## (2) INFORMATION FOR SEQ ID :647:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double

40

329

## (xi) SEQUENCE DESCRIPTION: SEQ ID :642:

AGAGGACAGA AAGGAACAGA ATGATCTTCC TACNCACAAC ACAAACGTCA 50  
5 GTTAATGTTC CATCCATGCT GCTTAAA 77

## (2) INFORMATION FOR SEQ ID :643:

10 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 127 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear  
15

## (xi) SEQUENCE DESCRIPTION: SEQ ID :643:

20 CCAGCGCCGA GAGCAGCCCC AGTAGCAGCN CATGGCCGGG TCCAACGCCT 50  
ACATCGACAA CCTTCATGGC GGACGGGACC TGTCAGGACN GGCCATCGTG 100  
GGCTACAAGG ACTCGCCCTC CGTCTGG 127  
25

## (2) INFORMATION FOR SEQ ID :644:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 116 base pairs  
30 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear  
35

## (xi) SEQUENCE DESCRIPTION: SEQ ID :644:

GTAGCCAGAC CACAACACCG AGTTGTACCC AGATAGCTGG GATTGGAAGT 50  
40 GAGGAGGTTT CTCACCCAC AGATAACCCA AGACACAAAT GTGCAATTAA 100  
AAGTTTATTT TAGACC 116

328

CGGGATGCAT GTGCAGGCAT GGAGTCATTG TCACATCA

138

## (2) INFORMATION FOR SEQ ID :640:

5

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 80 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :640:

15

CCGACCACCC CTCCTTTTC TTCGTCCATC CAGCACAGCA AGACCAACGG

50

GATTCTCTTC TCGGGCCGCC ACCGCGTGGA

80

## (2) INFORMATION FOR SEQ ID :641:

20

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 100 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

25

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :641:

30

AACTAACTG TTACCTTCCC TCGCTCCACA GAAGAAGACA GCCAGCTTCA

50

GGGGTCCCTG TTGCTGGCCA AGCCAGTGAG CCTGCTGGGA GGCTGGTCCA

100

35

## (2) INFORMATION FOR SEQ ID :642:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 77 base pairs

(B) TYPE: nucleic acid

40

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

327

## (xi) SEQUENCE DESCRIPTION: SEQ ID :637:

CCGAGCACGA GACCCTGATG CACATTCTAA AATAAAAGAA TGATGCACAT 50  
5 TTTAATAAAG CACAGCACAA 70

## (2) INFORMATION FOR SEQ ID :638:

## (i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 160 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

## (xi) SEQUENCE DESCRIPTION: SEQ ID :638:

CCGAGCANAN TCTAACCCGG CCTTGGACGA CCCGACGCCG GACTACATGA 50  
20 ACCTGCTGGG CATGATCTTC AGCATGTGCG GCCTCATGCT TAAGCTGAAG 100  
TGGTGTGCTT GGGTCGCTGT CTACTGCTCC TTCATCAGCT TTGCCAACTC 150  
25 TCGGAGCTCG 160

## (2) INFORMATION FOR SEQ ID :639:

## (i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 138 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

## (xi) SEQUENCE DESCRIPTION: SEQ ID :639:

CCGAACAAAT GTACGGAATG TGTGAGTCCC TCTGGAGCCC AACATGGATC 50  
40 CGGATCACCT GTTTGAAACC ATCTCCCAAG CCATGCTGAA TGCTGTGGGC 100

326

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :635:

10

CCTGCNCCGA TGCACCCGCC ATCCAGCCTG TCCTTTGGAC CACGCCACCC 50  
CTCCAGCATG GTCACCGCCA TGGGTTAGAN CCCTGCTCGA 90

15

## (2) INFORMATION FOR SEQ ID :636:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID :636:

CAGGAGACAC AGACAATAGT CACTACATCA CAGCCTTGTT CTTTCCGAAG 50  
GATAAAATGT CATTCAAGAA TGGGGTGAGG TGTTAGAGG GACTAGGTAC 100  
T 101

30

## (2) INFORMATION FOR SEQ ID :637:

35

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

325

AGAAAGGCAT CTTTCGCCAG TGGATTCGCC TCAAGGTTGA GGCCGCCATT 150

GGAAGATGAA A 161

5 (2) INFORMATION FOR SEQ ID :633:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 97 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :633:

CCTGCNCCGA CGATGCCAG AATCCAGAAC TTTGTCTATC ACTCTCCCCA 50

ACAACCTAGA TGTGAAAACA GAATAAACTT CACCCAGAAA AACAAAC 97

20

(2) INFORMATION FOR SEQ ID :634:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 178 base pairs

25 (B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :634:

CCAGCNCCGA AGCATTGGAT GCTTGACAAA CTAACGGGTG TATTTGCACC 50

35 TCGTCCATCG ACAGGTCCCC AGAAGCTGAG GGAATGTCTT TCCTCTGATC 100

TTCTTCCTCA GGAATAGACT CAAGTATGCG TTGACTGGAG ATGAGGTAAA 150

GAAGATATGT ATGCAACGTT CATTCAAA 178

40

(2) INFORMATION FOR SEQ ID :635:

324

(xi) SEQUENCE DESCRIPTION: SEQ ID :630:

CCAGCNCCGA AAAGCCAAGA CTTTCATCAAC TACATAGGTC TTACCATTGA 50  
5 CCTAAGATCA ATCTGAACTA TCTTAGCCCA GTCAGGGAGC TCTGCTTCCT 100  
AGAAAGGCAT CTTTCGCCAG TGGATTCGCC TCAAGGTTG 139

(2) INFORMATION FOR SEQ ID :631:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 117 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :631:

20

CCACCGCCCC GAGCGAATGT AACCCGGCCT TGGACGACCC GACGCCGGAC 50  
TACATGAACC TGCTGGGCAT GATCTTCAGC ATGTNCNNCC TCATGCTTAA 100  
25 GCTGAAGTGG TGTGCTT 117

(2) INFORMATION FOR SEQ ID :632:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 161 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :632:

CCAGCNCCGA AAAGCCAAGA CTTTCATGAAC TACATAGGTC TTACCATTGA 50  
40 CCTAAGATCA ATCTGAACTA TCTTAGCCCA GTCAGGGAGC TCTGCTTCCT 100

323

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :628:

10

AAAAGAAGTA GGTCTGTCTG TTCTGGTTGC CCTAAGAGAA GAAGANNNCG 50

GTGGCCACCT CGAGGTTAAG AGGGATATCA CTCAGCATAA TGTTAAGTGA 100

15

CCGGCAGC 108

## (2) INFORMATION FOR SEQ ID :629:

## (i) SEQUENCE CHARACTERISTICS:

20

- (A) LENGTH: 95 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID :629:

30

TCGCACCACT AGAAANCACC GTGACTGAGA AGAATGATGT GACCTTCAGA 50

CTTGACCCNN GGACAATGNC AGCTCCCAAT GNCCGTCTAG TGGCA 95

## (2) INFORMATION FOR SEQ ID :630:

35

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 139 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

322

(xi) SEQUENCE DESCRIPTION: SEQ ID :625:

AACAGCACGG AGATTGCGTT TATATATCAG ACCAAGCTC

39

5

(2) INFORMATION FOR SEQ ID :626:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 72 base pairs

10

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :626:

CCAGCGCCGA GGTGTATAT TTCTAGGTGC AGGTATATGA TTGCCATATA

50

20

ATAAAAATCT GAAAACATCC CC

72

(2) INFORMATION FOR SEQ ID :627:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 153 base pairs

25

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :627:

CCTCCGCCGG AGCTATCTGC ACTACATCCG CAAGTACAAC CGTCTTCGAG

50

35

AAGCGCCACA AGAACATGTC TGTACACCTG TCCCCCTGCT TCAGGGACGT

100

CCAGATCGGT GACATCGTCA CAGTGGGCGA GTGCGGCCTC TAGACAAGAC

150

40

AGT

153

(2) INFORMATION FOR SEQ ID :628:

321

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :623:

10

TTTATTGTAT CATGAGGCAT TGAAACATCT GAATAAATCA ATGTCTGGGC 50  
GGTGAAGGCA GCTGCTTTCT CCTTCACTTC TTTGGGTTAC TAGAGCAACT 100  
TGTCAGTAGA TT 112

15

## (2) INFORMATION FOR SEQ ID :624:

## (i) SEQUENCE CHARACTERISTICS:

20

- (A) LENGTH: 119 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID :624:

30

ACTCCTTCTG CCCCCGTTCT TCTAGTGAGA GGGGCGGACA AGGGGGCGGC 50  
GAAAAGAGGA GAAAGGAGAG AAACAAGAGT CGAGGGGGAC AGGGGAGTCG 100  
AGGTCTGCAT CCCCTCCCC 119

35

## (2) INFORMATION FOR SEQ ID :625:

## (i) SEQUENCE CHARACTERISTICS:

40

- (A) LENGTH: 39 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

320

AGTCCGTACC CTCAGTAACA GTGTAGTAGC TCTTCCTGT

139

## (2) INFORMATION FOR SEQ ID :621:

5

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :621:

15

TTCAAAAACA ACTTTATTCA TGACACATAT TAANNNAAAA CCCCACCCCT

50

GGAAATGAGC TAAAAAATA AACAAAATCC ACCTCCCACC TCCCTGNNCC

100

CACTTCCTCC CATGCCCTCC AAA

123

20

## (2) INFORMATION FOR SEQ ID :622:

## (i) SEQUENCE CHARACTERISTICS:

25

- (A) LENGTH: 173 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :622:

CACCCAAGAC CATCCTTTAT TGTAGTATTA GTTCATGGTA ACTGCATGAA

50

35

AAAACATTTC NNGAGGAATT TTCAATTTC AGCTTAAAGA ACNNNCCCAC

100

CAACATAACC AATTTATGAA ANNNAATTCA TTAAAAGGTA TAGAACCTCT

150

TGTNNNCATG ATGGCAAGGG ACA

173

40

## (2) INFORMATION FOR SEQ ID :623:

## (xi) SEQUENCE DESCRIPTION: SEQ ID :618:

5 TCTTCTTACT ACACTGGAAG TCTGAACTGG GTGCCTGTTA CCGTCGAGGG 50  
TTACTGGCAG ATCACCGTGG ACAGCATCAC CATGAACGGA GAGGCCATCG 100  
CCTNCNCTGA GGNCNGCCAG GCCATTGTTG ACACCNNCAC CTCTCNNCTG 150  
10 ANNNNCCCAA CCAGCCCCAT TNCCAACA 178

## (2) INFORMATION FOR SEQ ID :619:

## (i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 73 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID :619:

ACCACCCCTT CCTTTTCTTC ATCCAGCACA GCAAGACCAA CGGGATTCTC 50  
25 TTCTGCGGCC GCCACCGCGT GGA 73

## (2) INFORMATION FOR SEQ ID :620:

## (i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 139 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

## (xi) SEQUENCE DESCRIPTION: SEQ ID :620:

40 TGCCTTACAC ACTCAGGGAG ACCTCGGGTT GTACCTAGGC CTAGTGGACA 50  
AACTTTGGTA GAGGGTTCGG TACGACTTAC GACACCTGGC CCTACGTCAT 100

318

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 137 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :616:

10

TCTAACTGAT TTCAAAGCAA ACTCTCTCTT AATTAGGCTG CCTCTCCAGG 50  
GGAAATTTAG TGGCAGGGTC CCAGTGAGCC TGTAAGAAGT GTTCTACTCA 100  
CCAGAGTCAC TACTCCAGGT TGAGGACATG AGGCAGG 137

15

## (2) INFORMATION FOR SEQ ID :617:

## (i) SEQUENCE CHARACTERISTICS:

20

- (A) LENGTH: 139 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID :617:

30

GCAGGGCAGT CTTGGTGTGC AGCCCCTCTC CTCTCTGTCC CCTGACACTC 50  
CACAGTGTGC CTGCAACCCA AGTGGCCTTA TCCGTGCAGT GGTGGCAGTT 100  
CAGAAATAAA GGGCCCATTT GAGGGATGAC CGCATTCAC 139

35

## (2) INFORMATION FOR SEQ ID :618:

## (i) SEQUENCE CHARACTERISTICS:

40

- (A) LENGTH: 178 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

317

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :613:

TTGAAGCTGG GAGGCAGAGG TTGCAGCGTG CAGAGTCGTG CCACTGCACT 50

CCTGGGCGCA CAGCGAGACT GTCTC 75

10

(2) INFORMATION FOR SEQ ID :614:

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 25 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :614:

ACGGGATTCT CTTCTTCGGC CGCCA 25

25

(2) INFORMATION FOR SEQ ID :615:

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 72 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :615:

GCAGTGTACT ATGTTTCGCAT CTGTGAATAG CCACTGCACT CTAGCCTGGA 50

TAATATAGTG AGAACCCATC TC 72

40

(2) INFORMATION FOR SEQ ID :616:

316

GGAATGTTAT CAAAAGCACA TTAAGTGGTC AAAGCCAGAT ACAGAAGAGT 150

AGGTATGATT TTATAGGNAT AA 172

5 (2) INFORMATION FOR SEQ ID :611:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 51 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :611:

TCCACCTTAC AGACCTGATT TGGCTGCTTC TGACGTCTGT TTCCTAATCT 50

T 51

20

(2) INFORMATION FOR SEQ ID :612:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 60 base pairs

25 (B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :612:

CGCCTGAAAC TTTGAGGATA AACTTTTTCA AAAAAATAAA ACAGTATCTC 50

35 TTAATCACTG 60

(2) INFORMATION FOR SEQ ID :613:

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 75 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

315

TTTCCTACAC ATAAAGTAGT GAGAACATCA TCCTATAACA GGGAAGTGTG 100  
ATTATTTAAA AAACGCAGAA CTTATTTATT TGGCTTTAGA AATAACTGCA 150  
5 TACAATGTCA TAAGTCGAAA AGAACTCAAA ATAA 184

## (2) INFORMATION FOR SEQ ID :609:

## (i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 191 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear
- 15

## (xi) SEQUENCE DESCRIPTION: SEQ ID :609:

GGGGACAGCT NNNNNGTTGT TTTGGAGCCT GTTGACTTTG TATTCTCTGC 50  
20 CTGTGATTTT CNNTTCTAAA TGAAACTCCA TGTNNNAACC AGGACGAAGN 100  
TGAGAAGGAA AACGCCAAAT GCTTTGGTTA TTAGAGNTTA ATAGGNAAGC 150  
25 TCTGTTACAC TAGGTGTAGA GTTCCAGAAT GTTCTTTTGT T 191

## (2) INFORMATION FOR SEQ ID :610:

## (i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 172 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear
- 35

## (xi) SEQUENCE DESCRIPTION: SEQ ID :610:

GCAACTGTGC AAACATCCAT CAGTGTGGAG GAATGGTAAA CTTGGTACAT 50  
40 GCATGCANTN GNNNCATATT TTTGTGGTTA AGATNNTGAT GTATAGGCAT 100

314

AATAAAGCAT TCTCACAACC TTTGTTGGGT CAATGATTCC TTTTACCAC 50  
ANNTACAGAA TCTCCACCAT AGCATCAAAA CCAACTCTGA GGAACCTCGC 100  
5 ATAATTCTTA ACTACAAAGA TCCTTCAACA CCCGCATTCT TACAATGTCA 150  
TCGCCGGAAT TTTGAGTGTT CTTTCAATAA CCTACANTA 189

## (2) INFORMATION FOR SEQ ID :607:

10

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 171 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 15 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :607:

20

GGAAAAGNTC ATTACATAAG CACCAAGNCA TTGATTATGA TCCACCGGAA 50  
GAGCTCGTAT TTATCCTTTG CTTTNATNTG AGACCAAGCT AGCCCTGAGT 100  
25 AATTTTANNT GGTTCCTAAA ACATATGGCT TATCGTACTC TAAGAAAAAT 150  
GCCTTACGCA CATTCCTTTN T 171

## (2) INFORMATION FOR SEQ ID :608:

30

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 184 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 35 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :608:

40

GGAAAAGTNC GCATATAGCG TGCNATAATA CTACGNCTAA GGAGAAACAA 50

## (xi) SEQUENCE DESCRIPTION: SEQ ID :604:

5 GACATCTGAT CATCTCACTG GACGCCACAG GGGCAAGAGG GTGGTTTTC 50  
TGAAGCAGCT GGCTAGTGGC TTATTACTTG TGA CTGGACC TCTGGTCTCA 100  
ATCGAGTTCC TCTACGAGAA CACACCAGAA ATTTGTCATT GCCACTTCAA 150  
10 CAAAATCGAT ATCAGCAATG TAAAAATCCC AAACATCTTA CTGATGCTTA 200  
CTTCAAGAAG AAGAGCTGC 219

## (2) INFORMATION FOR SEQ ID :605:

15

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
20 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :605:

25

AGCGAACACG AGCACAGCGA GCGCACAGAG AGCAGCAGGG AGGGCAGCCA 50  
CCGCCGGGAC GCCGGCAGGG GCACGAGAAG GCAAGGAGCG GACACCCGNG 100  
30 NNGA 104

## (2) INFORMATION FOR SEQ ID :606:

## (i) SEQUENCE CHARACTERISTICS:

35

- (A) LENGTH: 189 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
40 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :606:

312

## (xi) SEQUENCE DESCRIPTION: SEQ ID :602:

	GGAAGAGAAC ACATACACGA GGACCAGTAC CTGATGAGGA CAAGAGAGAT	50
5	GGGAANNNGC TGTGGAATTC CTTTCGGCAC CCTGGATGTT AACCCCTGCT	100
	CAGGAAAGGG TGCATCTGTC TTCATCATGC CTCTCTCTCC TCCTCCTCCA	150
	GCCACCTCCC AAAGGCAGAG CTGCCGCAAC CTGCCTGGCC ATGTGGTGGC	200
10	AAGTACCCAG TAGGAG	216

## (2) INFORMATION FOR SEQ ID :603:

15	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 213 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear
20	

## (xi) SEQUENCE DESCRIPTION: SEQ ID :603:

25	GAAAAAACAA TCATGACAGC AACTCTCCTA ACCACAAAAA TCACATATGT	50
	TATCTTTCTT TCAGGACTAA TAATTAATAT TTAAGAGGAA AGCACATCAA	100
	TTTCTAGGGC CCTTCTTGGG GAAAGGTTCA TATAATTTAG CATACATACA	150
30	TATTCAGTGA ATGCATTCAT ATATTACTAT ATAAACACTC TCAGCTACAA	200
	TGGTAATATA ATG	213

## (2) INFORMATION FOR SEQ ID :604:

	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 219 base pairs
	(B) TYPE: nucleic acid
40	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

311

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :600:

ACAGTGTGTG CCCTGTCAGC TCCGCAAATT GGCAGTCACT ACGTTTGTGC 50

CCCCTGTAAC CTTGTGATCT TCACTGCCAC TAGCGATGAA GTCTTCATTA 100

10

TGGCCTC 107

(2) INFORMATION FOR SEQ ID :601:

15 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 173 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :601:

25 ACTGCTAGTG AAATTCACAT GACTCACAAT TCCCTTTAGC CAATGTTACC 50

GAAGTCAGTG TCAAGAAAAC TTAACAGAAA AAAAAAAGCA CAGAGTGAGT 100

TCCTACCATA AAAATCCAGG CTGCCCTGTT TCCTAGCTCT AATATAAGCC 150

30

ATTTTCTTTC CTTAGTGAC CAA 173

(2) INFORMATION FOR SEQ ID :602:

35 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 216 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

40

310

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :598:

ACAAAACGCA GATATAAAAA AGTTACAAAG ATTTTATAGAT TTTCATTAC 50  
10 AAAAAAAGTC ATTACATTT TACACTATAC ACGTTATGAT ATAATACAGG 100  
AAAGTATTAT GTGCATTGTA AGAGAAGGAA AATAGAACTA CTAGATCACA 150  
15 CGTGTTGTTC TGTGCTCTAA AATACCTAAA GGTGGATTCA TTTAATGCAA 200  
CACCAGGGAC 210

(2) INFORMATION FOR SEQ ID :599:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 116 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
25 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :599:

30

AAAGGAGTTG AGTACTGTAA ACGCAGAGCT ACATAGAAAA AACGGGCTTC 50  
AAAAATCTGC ACAGAGGTTT GCTTGAGAAT TTAGCTACAC AAATATGTGT 100  
35 AGAAGTGAAA AAAAAA 116

(2) INFORMATION FOR SEQ ID :600:

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 107 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double

309

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :596:

	GACAAACTGT TGACACCCGG AGGCCTAAAC GAGGATTTC A GCTTCCATTA	50
	TGCCCCAACTC CAGTCCAACA TCATTGAGGC GATTAATGAG CTGCTAGTGG	100
10	AGCTGGAAGG GACAATGGAG AACATTGCAG CCCAGGCTCT GGAGCACATT	150
	CACTCCAATG AGGTGATCAT GACCATTGGC TTCTCCCGAA CAGTAGAGGC	200
15	CTTCCTCAA GAGGCTGCCC GAAAGAGGAA ATTCCATGTC ATTGTAGCAG	250

(2) INFORMATION FOR SEQ ID :597:

	(i) SEQUENCE CHARACTERISTICS:
20	(A) LENGTH: 225 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :597:

	CTGCCAAATA CTTTCTTCAC CAACTCATGA GGAGAGGGAA CATGCTGAGA	50
30	AACTGATGAA GCTGCAGAAC CAACGAGGTG GCCGAATCTT CCTTCAGGAT	100
	ATCAAGAAAC CAGACTGTGA TGA CTGGGAG AGCGGGCTGA ATGCAATGAG	150
35	TGTGCATTAC ATTTGGAAAA GATGTGAATC AGTCACTACT GGA ACTGCAC	200
	AAACTGGCCA CTGACAAAAA TGACC	225

(2) INFORMATION FOR SEQ ID :598:

40

	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 210 base pairs

308

(xi) SEQUENCE DESCRIPTION: SEQ ID :594:

	GACCCTAACA ATATGTACAA AAATATAAAA TGTAATAAAA AAATACAAAC	50
5	AAATTTCTT TTTAAAGTAC TTTAAGAAA AAAAGCAGGG CCTTGAAGT	100
	TTTGGTTCTT TTTCTCTCCC CTGTTGCAA TTCTCATGGT TTGGGTTGGG	150
	TGGTGGAGAG CGCGTGTCTAT CTGCGGGTGC CTGCCCACGT GGGCGGGCGG	200
10	CTCTCTACTC GAAGG	215

(2) INFORMATION FOR SEQ ID :595:

15	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 272 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear
20	

(xi) SEQUENCE DESCRIPTION: SEQ ID :595:

25	GGGGCTGGTT TGGTCATCCG AGATCATTA AAATGGCTGA CCCTAACAAT	50
	ATGTACAAAA ATATAAAATG TAAATAAAAA ATACAAACAA ATTTCTTTT	100
	TAAAGTACTT TTAAGAAAAA AAGCAGGGCC TTGGAAGTTT TGGTTCTTTT	150
30	TTCTCTCCCT GTTGCAAATT CTCATGGTTT GGGTTGGGTG GTGGAGAGCG	200
	CGTGTCATCT GCGGGTGGCA CTGCCACGGT GGGCGGGCGG GCTCTCTACT	250
35	CGAAGGTGAC CACGTTTAGA TT	272

(2) INFORMATION FOR SEQ ID :596:

40	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 250 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double

307

CATGTTTCCTT CTATGANCTN CGTGGNATAT AGGCATATTT ATTAATGCTA 300  
TTTANGGCNT NNGTGCTTTG TAATGATTCTG NCNTTAGGTG AAGGGNTACT 350  
5 TTTNTNNTNC TTCNTAGTAG ATTNNGNTTN NTCTTTTAA GAGGANTCNA 400  
NTTTCATGNG TAANCATCAT CTTTT 425

(2) INFORMATION FOR SEQ ID :593:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 258 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :593:

20

CGCTGCATGC GTCAGCGCNA CGCGACGACA GCGCGCGCGA CGCGCGCGAC 50  
GCACAAAANA AATGCATGCC AACACGAANA TATGTGCACA CAAACGCAAA 100  
25 CGCGTGTGAA CACATGCGCG CNNGCGGCNC GCGATNCAAA GCTGAAATGT 150  
GCNNGNCNGT CGTGNGCGNA AATGTGAAAT GAACAAACAA CAATGAATGA 200  
ATGAATGTGA AAAAGAGNGN GNTTGAAAAT TNTANAGNNC CCCCCNTNA 250  
30 ANCAAAAAG 258

(2) INFORMATION FOR SEQ ID :594:

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 215 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
40 (D) TOPOLOGY: linear

306

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 247 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :591:

10

ATTCGCCCNN TAAGTAAGTC GTNATTANAC GCGACGNCTA CTA CTGAGAC 50  
NCGCATGCGC TCTCTCTACA CTAAAGCTCG TCGCTNGNTN ACTTGCGNGN 100  
NAAAAAAACC CCCTGGGNNC GCTTTTCACC CCCAACTTT CAAATTCCGC 150  
CCCTTTNGGC NANGCCCAAC CANNCCCCC CCCTTTTNC CGNCCCANNC 200  
TTNGGNCNTA ANNATTNAGN CGGNANGNNN GGGCCCCCGG CCAACCC 247

20

## (2) INFORMATION FOR SEQ ID :592:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 425 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :592:

GGAGGGGAGT AGAGGAAATT TTCATTCTGG AAAAAAATGC ATACTGTTTG 50  
ATATATTACT CNTCATGCTT TCCACAGATA TTATACACAG ATATTATATT 100  
CCANGGATTA CGTTGCAATG TCTTCAAAA TAGANAATTC ATTTTATATT 150  
TCTNGATGAA ATATAATAGT ANCTNNGCTA CTTTGGGAA TGTGACAAAA 200  
TACTATGATG ATTACAACTC ATTAAAGCAT AAATNTGCAT GATTTAAC TN 250

40

305

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 184 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :589:

10

GAGAGAGAAC ACTCCCCTCC ATCCCAGCAC TATGCACAGT TCACGGCTCA 50  
TATGCAAAGT GGAAGACACG TGGGACAAGA GCAAAGCACA AGTGACACAT 100  
GGTCCCTCTC TAACACCTCA GCACACCAAC CCTGACGCTC CCATCACAGA 150  
TGCTGNTCAT TCTTNCACGG NCCCCTTTTA TAAT 184

## (2) INFORMATION FOR SEQ ID :590:

20

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 243 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID :590:

30

GGGGGCCCCG CGTNCACNCC CCCACACTCT TGGTAGGCAA TGCTTGTCCTCC 50  
NATATAGTTG NNGTCCTATC GAGTGACACT CTCGTTCATG GATANGGTGN 100  
GTAAAACCCN TNGTNGCATC CNNATTGGGN GCANTGNGCC TNTCCCCCTN 150  
AANGGTTTTT GCNTNCACTC GACCTNGGGA GGATTCAATG NACNNNCTNG 200  
CANTGGNCAA GCNTTGNTTG CNNGNATTGA GAACCCNCCA ATT 243

40

## (2) INFORMATION FOR SEQ ID :591:

304

AGGTCAAGTC TACAGCTGGA GACACCCACT TGGGNGNANG AAGATTTTGN 50  
ACAACCGAAT NGTCAACCAT TTTAATTGCT GAGTTTAAGC GCACNTTAAA 100  
5 GAAGGACATC AGNGAGAACA AGAGAGCTGT AAGACGCCTC CNTACTGCTT 150  
GTGAACGTGC TAAGCGTACC CTCTCTTCCA GCACCCAGGN CAGTATTNAG 200  
NTCGNTCTNT CTATGAAGGA ATCGACTCTN TACTCCATAC CNNNCCGATT 250  
10 GAGACTGATG TGACNTTCCT GGGACTGNCA 280

## (2) INFORMATION FOR SEQ ID :588:

15 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 371 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear  
20

## (xi) SEQUENCE DESCRIPTION: SEQ ID :588:

25 GGTGAAGAAA CTCCAGATAT CAAGGAATTG GGAAATCCTG GGCCAAACCA 50  
CCCCAAGATG ATTACACTGA AATGTAGTAT TAGTACTNCT GCCAGATCTC 100  
TTTTTAACAT CATGTGCGTC TCTTGGGATC CAGCAAAGT GTTAAGCCAC 150  
30 AATGCCCTTG TGCCTTTTAA TATACCACAG TGCCAGTTAA ACTAATATTT 200  
TNTTTTGTTG CTTTTTGGGG TATTTTCATT AGTATTTTCAG CAAATCTCAT 250  
35 GATAAAGGNC AAGGNCAAGA ACTNCAGAGN ACTGAGCAGA GAGGCTNGTG 300  
ATGAAANGTG AAGGCTTCNA CTGACTTTAN GCAGTGGCAG TCANGNTACT 350  
GNGNNGCANG CTTANCTATG A 371

40

## (2) INFORMATION FOR SEQ ID :589:

## (xi) SEQUENCE DESCRIPTION: SEQ ID :585:

5       ACCCACGGTA CTTACATCCT ATGATATGGC CTGCAAATA AACTACAAAC       50  
      GCACTCACAT CGCTATAATC CTTTAAAGGA CTAAACTTT ACTCCATTAA       100  
      GACTTTTATG ACTTCTAACA ACCTCGCCAA CCTCCTCACC CCCCCTATA       150  
10       CCTCGGAGAA CTTTCGCGTA ATAACCACGT       180

## (2) INFORMATION FOR SEQ ID :586:

## (i) SEQUENCE CHARACTERISTICS:

15       (A) LENGTH: 183 base pairs  
      (B) TYPE: nucleic acid  
      (C) STRANDEDNESS: double  
      (D) TOPOLOGY: linear

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID :586:

25       ACCGACATCA CGANNGACTT GGTCTTAGTT GAGCAATTG GCTAANNNNN       50  
      NTNCTNNTTA GCACGTTCTG AGTCTGTGGG ATAGCTGCCA TGAAGTAACC       100  
      TGAAGGAGGT GCTGGCTGGT AGGGGTTGAT TACAGGGTTG GGAACACTCG       150  
30       AGANTGGCAT CCTGCATATA CTGGTTAGTG AGG       183

## (2) INFORMATION FOR SEQ ID :587:

## (i) SEQUENCE CHARACTERISTICS:

35       (A) LENGTH: 280 base pairs  
      (B) TYPE: nucleic acid  
      (C) STRANDEDNESS: double  
      (D) TOPOLOGY: linear

40

## (xi) SEQUENCE DESCRIPTION: SEQ ID :587:

302

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :583:

GGAACAAAGA AAATGTACAG AGTTATATGC GCTTTTTTTT GGTATGGGGG 50  
ACAAGAAACA CTTACCAACA AAAATATTTC AACAAACCCA AAATAACTTA 100  
CTCACAAATA TGCAAATTA TCTATGGCAT AGTATTTCGC ACTCGATGAC 150  
ATTTAGAGAT AAAAAATCAA ATGGAGCTT 179

15 (2) INFORMATION FOR SEQ ID :584:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 186 base pairs  
(B) TYPE: nucleic acid  
20 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :584:

AACTGCCATG AAGTAACCTG AAGGAGGCGC TGA CTGGAGG GATTGATTAC 50  
AGGATCGGAA CACTCCACAC TCGCCATTCT CTGCATATAC CGGTTAGCGA 100  
30 GGCGAGCCTG GCGCTCTTCT TCGCGCTGAG CTAAAGCTAC ACACAATGCT 150  
TTGCGACCAC AATNCACCCT TCATTTCGTA ACTGCT 186

35 (2) INFORMATION FOR SEQ ID :585:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 180 base pairs  
(B) TYPE: nucleic acid  
40 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

301

## (2) INFORMATION FOR SEQ ID :581:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 242 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :581:

CGGAGGGCCC TGT TTGGGAA AAATAGGATT TTAAAAATAT GGTTCATTAA 50  
TTTAGGTTTT CTAACATCTA CTTGGGGATG TAGCCTCCAG TGAGGTCAGT 100  
TAAGTGGGAC AGAAACGGCA GAGGGAAGAG GTCTTTGCTT CCCCTGGGCC 150  
CATTCTCCCT GGCTGCCAGC CCTTGAAGTC AGAACACCAT GGGAAAATTC 200  
AGGAGTCGGC ACTGTAGCCG TCAAGTGGCG CTACTTTCCA CA 242

## (2) INFORMATION FOR SEQ ID :582:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :582:

GCATTTTTCT TGTGTGCTGT TTATAATAGC AAAGCAG 37

## (2) INFORMATION FOR SEQ ID :583:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 179 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double

300

TCTCTNNAAT ATTTGCCTGT AGGTAAAAGC AAGCTCTGCA TATCTGTACC 250  
TCTTGAGATA GTTTTGT TTTT 270

5 (2) INFORMATION FOR SEQ ID :579:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 139 base pairs  
(B) TYPE: nucleic acid  
10 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :579:

GAGTTTTCAG AGGCCCGTGA GGACATGGCT GCCCTTGAGA AGGATTATGA 50  
GGAGGTTGGG TGGATCTGTT GAAGGAGAGG GNAGAAGAGG AGAGGAATGC 100  
20 TAAAGTTAAA ACGTAATAAA GATGCTGCTC TTACGGAAG 139

(2) INFORMATION FOR SEQ ID :580:

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 168 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :580:

35 GGCAGGAATA CATATAGTCA TCATTGCCAG ACTTAATATG AGAGGTGAAA 50  
TGTTGATCC AATTTATTTT TTGATAAGT TTTTCTTTCC TATNCCTNTN 100  
GTTTTGATAA TATAATAAAG AAGATGAGGG GCCCA A TATAGAGCTC 150  
40 CTGAGNGAGT TTTNGGAG 168

299

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 255 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :577:

10

GGACCTTGAC CCACATCCAT GTTGAGGAAT GTCCTCTTGT CAAGGTCAGG	50
GAACAGCACC CACAGAGGGC CTCTGGGTCC CTCTCTGCTC AACTCCCTCT	100
CTCTCGGTTC CTGCGAGGCT CATAGGGTGC AGGGCCCAGC AGAAGGACTG	150
AGTCTTCCTC CTGGACTTCT GGTCCTGGTA GGCTGTGCTT CATGCTCTCC	200
TGTCACCTGT ACTGTAAGGA ACTATTATGA CAAACGCATA AAGAATATGA	250
CTTTG	255

20

## (2) INFORMATION FOR SEQ ID :578:

25

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :578:

35

GAGGAGTCCA TGCCATCCTT GATGGAAAAG AACTGAAGA GAAAAGACAG	50
CCTGTGGAAG AAGCTCAAAG GTTCTTTGAA GAAGAAGAGA GAAAATATGA	100
CATGATATCT TTGCTTTTGA GTTCCTCAGC CTCTCTGAAT TTATTAGTTG	150
GACAATTCCA TATGCAGCAT TCTGCTTCAA TATANCTCTT NNGGTCTCTC	200

40

298

ATTATGGGGC AGAGAACCTT TTAATAAGTC TCATTAAGAT CTGAATTTTG 250

GTTCTAAGCA TT 262

5 (2) INFORMATION FOR SEQ ID :575:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 56 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :575:

CCAAGGAACC ATCTGCGCCG CAAGCCAGAC CCCACAAGAC CTAGNTTGGT 50

CCTGAC 56

20

(2) INFORMATION FOR SEQ ID :576:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 158 base pairs

25 (B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :576:

GCGAGTCTCA AAGAGTAGAG GAGCGTCTAC TATCTTTCAA CTCCGATCTT 50

35 CTGATGNCGG ACTTTACCGT GACAGCGAAG TGGTATTGTA CGTCCAGGCC 100

CGCCAGCCAC TGTCTTCATG CAGGAACCAC AGTGCCAGAT CCCCACAGCT 150

CGTATCTT 158

40

(2) INFORMATION FOR SEQ ID :577:

297

CTTTCCTGTT TTAAACATGA AAGTGTGGC

179

## (2) INFORMATION FOR SEQ ID :573:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 189 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
10 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :573:

15 AGGACCTCTA AGACATCCTT ATGACGACAG TTTTGTCCAA GGGGATATCC 50  
ACAGAGTACC TTGTGGCATT AGGTGATTGT AGTCATACAC TTTAAAAAGA 100  
TTTTATTTCT GATCTTTTGG CGATCTTCTT CTGCCCATG NNGCTGTTAC 150  
20 TTNGCNCGGG NAGCGGTAA TTCTANCCGC TAGGTGTGC 189

## (2) INFORMATION FOR SEQ ID :574:

- 25 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 262 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
30 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :574:

35 GTGCCTTCTA GGTTTTGAAC TTCTATGCAT TAGCGCAGAT GTGGAATGCG 50  
TAAAGGTGTT CATAGTTTGA CTGTTTCTAT GATGTTTTTT CAAAGAATCG 100  
TCCTTTTTTG AACTATAATN CCCCNCGGTT ATTTTACCAT CACAGTTTAA 150  
40 ATGTATATCT TTTACGTCTC TACTCAGACC ATATTNAAA GGGGCGCCTC 200

296

NGAAAGATGA AATAGATTNT TGAGCACTGG NTGCAGAGCC AAAATGCNTA 150  
ATGCTTT 157

5 (2) INFORMATION FOR SEQ ID :571:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 193 base pairs  
(B) TYPE: nucleic acid  
10 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :571:

GGCACTAAAG CCTTTAATAA TACGAGATGA AATGCAACNG TGNNATGACA 50  
AGTAAGTGAG CCTGACCTGG CATTGCCTCG CCTCACCGCT GGCTTTGACC 100  
20 AGGGTATGAT CTTTAACTTT TCTGAGCTGA TTTGATCGTG GTCTTTACAC 150  
ACAGGTGGTC GTTCCTGTTT GGACACTGTT TTATTTGTTT GAC 193

25 (2) INFORMATION FOR SEQ ID :572:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 179 base pairs  
(B) TYPE: nucleic acid  
30 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :572:

TCGCAGGAGA AAGAGGTTTT CAGAGGCCCT GAGGACATGG CTGCCCTTGA 50  
GAAGGATTTC AGGAGGTTGG TGGAATTTGT TGAAGGAGAG GGCGAGGAAG 100  
40 AAGGAGAGGA TACTAAAGTT AAAACGTCAC AAGGTGTGCT TTTAAGGGAG 150

295

AAACAAATAT AGTATAAACA TTAAACAAAT GAACAATAAT CATCAATAGA 100

CGGGTTACTT TCAAGGAAGA GTTGTTTTGT GACAAATTCT ACTCTTGATC 150

5 TA 152

(2) INFORMATION FOR SEQ ID :569:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 181 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :569:

CAGGTCCGCG TGCTCTCCGC ACCACCCAC TTCATTCCGG CCAAACCAAC 50

20

CGCACCCCTG AATTTCTCCG CAAATTTCTT GCGGCAAGG TCCCAGCATT 100

TGAGGGGATG ATGGATTCTG TGTGTTTGAG AGCAACGCCA TTGCCTATTA 150

25

CGCGAGCAAT GAGGAGCTGC GGGGAAGTAC T 181

(2) INFORMATION FOR SEQ ID :570:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 157 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :570:

ATCCCTTGGG AGTTTATTCT CCTGGTAAGC TGTAATTGCA TATCCAGTTT 50

40

AACTGGACTG GGCTGTGTTG GGCGAGGATC NGCAGGGTTT TTCCTCNNT 100

294

GAAGATACAG AACCATCCGT GAAAATCATT TAGCACTGGA GACCTTCTTT 50  
GTATTACTTC CTNGTTACTA GACCTCTAA TTCAATGGGG CCCTGCTGGT 100  
5 TTGTCGATGA ATTGAGCAAC TGAGAACG 128

## (2) INFORMATION FOR SEQ ID :567:

(i) SEQUENCE CHARACTERISTICS:  
10 (A) LENGTH: 202 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

## (xi) SEQUENCE DESCRIPTION: SEQ ID :567:

GGAGGCTCGG GAGTAGCATC CTCAGGAGTA GTGTAGCGAG CAAATTGGA 50  
20 AAGTAGTCCT CAATCTTCGA TTTCCCAGCA AGGACTTTCT CAGCNAGCGA 100  
TCTCGNTTGT TGAGGAACGG ATCAAGAGAT GNNNGTNTAG CTGTNNTGTT 150  
25 GTTTAGATGT CTTGAAGAGG TTAGAGCCTC CTGTAGGCGG TTGGNNTGGG 200  
NG 202

## (2) INFORMATION FOR SEQ ID :568:

30

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 152 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
35 (D) TOPOLOGY: linear

40

## (xi) SEQUENCE DESCRIPTION: SEQ ID :568:

ATGTCATGAT GCCTAACTCA TAACTCTTT GCCTCAAATA TAATTACTAA 50

293

GGGACCCCAA ATCACATCCA GAATACTAGA GTGAGGCAGC TGCAACATGA 50  
CACAGAAAAA TGAATCAGG ATTTAGGGGA ATTGGATTTC AGTGCCTATT 100  
5 GAGACACGAT CTAGGAAGCC TACCACTTTG GCTGCTCACT GTATGCACAC 150  
AACCCNANNA NAATNGATGA AAACAAGAAT GTACAGCATG CTCCTAACAC 200  
AANGTGACTA TTC 213

10

(2) INFORMATION FOR SEQ ID :565:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 167 base pairs  
15 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :565:

TCCATCTGAC ATCGCATTTT CATAGAAATG GCCAAAGAAA GAAGGTCCTG 50  
25 GGGTTTTTCA TAGAAAGCTC AAAAAGTTCA ACCTTGATGC TATCCCCCAG 100  
CCCAATACAA AATACACAGA AAAAGCAATT ATTAAAATAC TGGCTTCGGT 150  
TTCTTTTTTT CCTTTAA 167

30

(2) INFORMATION FOR SEQ ID :566:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 128 base pairs  
35 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :566:

292

(xi) SEQUENCE DESCRIPTION: SEQ ID :562:

ATAAGTTATA GCAAATACAG TCTTCACAGA TTTGAGTAAC TTTATTCGAT 50  
5 TTTATAGTGA TTTCTTAAGG CCTATATCCA ATGAAACCAT TTCCAAGCTC 100  
TATGAGGAGT GGAATTTTAG ATGTCTATTA CATTNCTCTT TTAAAAGAAA 150  
AATGCTTAAC NNCTAGAATG AGCAAGATTA CTT 183

10

(2) INFORMATION FOR SEQ ID :563:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 187 base pairs  
15 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :563:

AGAGACACGT GAAATTCATA TCTCAAANNC ACAGAGCTGA GACTTTGGGC 50  
25 CTAAATACTG TACCACTGGT TCCCTGAACC AAGGAAGAAA AGTGTCGGTA 100  
AAGGCCCGTT AAGACAAGAT GGCAAGGAAA AGCACCTTAA ACAATGGTAA 150  
GATTTATGTT AGATCAGTGG TAAGAGTTTC TAGTGAC 187

30

(2) INFORMATION FOR SEQ ID :564:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 213 base pairs  
35 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :564:

291

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :560:

CCTTGATGAT ACCATTATCC TCATTATAGA TGATGCACGG GCCCCTGCGC 50  
TGGATACGGC GACGGTTTCT CATTTGCCTT TGTCAGCTCT CATTCGCTGA 100  
10 GAGGCATAGA CCTTTTTGAT ATCATCAGGC TTTCCGTTTT TAGGAGCAAA 150  
ACAGCTTCTT 160

15 (2) INFORMATION FOR SEQ ID :561:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 101 base pairs  
(B) TYPE: nucleic acid  
20 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :561:

GCAGTTGGCA GGTGCACTAT CCCAGATGGG CCACTAATAG AAAGTTCCGC 50  
AAATGCACCC CGTTCCCCTG TGCGAGATCG TTTGAATNAG ACCAGAACT 100  
30 G 101

(2) INFORMATION FOR SEQ ID :562:

35 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 183 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
40 (D) TOPOLOGY: linear

290

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 183 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :558:

10

GAATTTAAAA AAAAAGAAAG AAAGAAAGAA AGGTTCCATC TTAGATTCTC 50  
ACAACCTTCG TTCCGCAGTT CATTAAATCCG ACTCTGATGC TAAGGTGACA 100  
GTGTATGTAA GTAGATTTTT GTTTTCAGTG AAGGAGACCT GGGAAAAGAT 150  
GGATTTCTCT CTGTATCTTA AGAGTTATCA GAT 183

15

## (2) INFORMATION FOR SEQ ID :559:

20

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID :559:

30

GTCATCTTTG GAAAGTGAGA TAACCAAGGA AATAATCGAA GGAGTTAGGG 50  
AGATGATTAC GTGATAATGA CTTTGGGCGC TTAACCTTTG ATCCCGGGTA 100  
TGCTNAAGAA GCTGAC 116

35

## (2) INFORMATION FOR SEQ ID :560:

## (i) SEQUENCE CHARACTERISTICS:

40

- (A) LENGTH: 160 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double

289

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :556:

TCTGCTGTCT GTCGCAGGAG AAGGAATGTC AGAACTTCA TCCTCTTGTT 50  
GGGGAATGCA CCCTCNTGAG TAGGCTGACC CATGAGGCTG TGGGAATTGA 100  
10 GTCTTAGGAC ACAGAGACCA GGGTGTGAA TTTTCTTCCC TGCCCCTAGG 150  
CTGTTCAGGT CTTCTGCAG CAGTCAGGGC TGCAAGCCCT GGAAAGGCAT 200  
15 CAAAAGAGGC CCAGCTCCAG GATCGTGTGT ATGCTCTCCA GCAGACAGCT 250  
CTTCAAGGGT GATCTTGTT 269

20 (2) INFORMATION FOR SEQ ID :557:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 245 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
25 (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID :557:

ACTCCCTCAA GGTCGTGCGT CTAAGCCTAC AAGAAAGTTT GCCTATCTGG 50  
ACCTGNCTC ACGAGGTTGG CTGGAAGTAC CAGGCAGTGA CAGCCACCCT 100  
35 GGAGGAGAAG AGGAAAGAGA AAGCCAAGAT CCACTACCGG AAGAAGAAAC 150  
AGCTCATGAG GCTACGAAAC AGGCCGAGAA GAACGTGGAG AAGAAAATTG 200  
ACAAATACAA AGGTCTCAA GACCCACNNA CTCCTAGNTT NAGCC 245

40

(2) INFORMATION FOR SEQ ID :558:

288

## (2) INFORMATION FOR SEQ ID :554:

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 198 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :554:

ACTTATTGAA ATAGCAGACA TTTCGCTAGA CACTCCAATT AACCTGATAT 50  
15 GAGGCGCTAA TCAATAAAAA AAGTTAAACA TTTGCATGAC TCTACTATGG 100  
GAATAAATTA CCTGTTTAAT ACCTCGACTT TTTATAGAAA AATAATGATG 150  
NCCAAGGTAA ACCAGGTAAC CCAGGCCTGT GAACTATATG CCTGGAAC 198

20

## (2) INFORMATION FOR SEQ ID :555:

## (i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 97 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :555:

CAAGCTGAGG AGCAAGGAGA GCCAGTCTGA GTCCCAAAC TGAAGAACTT 50  
35 GAGTCTGATG TTCGAGGGCA GGAAGCACCC AGCACAGGAG AAAGATG 97

## (2) INFORMATION FOR SEQ ID :556:

## (i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 269 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double

287

AGGGCAGCAT TTTCATATCC AAGATCAATT CCCTCTCTCA GCACAGCCTG 100  
GGGAGGGGGT CATTGT 116

5 (2) INFORMATION FOR SEQ ID :552:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 150 base pairs  
(B) TYPE: nucleic acid  
10 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :552:

CTCATCCTCT CCTATTACAT AGTGAAGCCC ATGNCAAATA GGAAGAAGCT 50  
CAGTATCGCT CCTCCCACCA TAACCCCCCT TAATGCCTCC TGAACCATAG 100  
20 TTNCCTCCAC TATATATCCC CCCATGTTCC TGCTACCCCA AGTTTTCACT 150

(2) INFORMATION FOR SEQ ID :553:

25 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 189 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :553:

35 ACTTATTGAA ATAGCAGACA TTTCGCTAGA CACTCCAATT AACCTGATAT 50  
GAGGCGCTAA TCAATAAAAA AAGTTAAACA TTTGCATGAC TCTACTATGG 100  
GAATAAATTA CCTGTTTAAT ACCTCGACTT TTTATAGAAA AATAATGATG 150  
40 NCCAAGGTAA ACCAGGTAAC CCAGGCCTGT GAACTATAT 189

286

AGGGGGCTAA NGGTTGGGGG CAGGAGGCAT TGCTGATGAT CTTGAGGCTG 50  
TTGTCATACT TTTCACGGTT CACACCCACG ACGACACGGG GACTCAGCAG 100  
5 AGGGGCAAGA CACGACCTTT AGTTTCCCCC TTGCGATAAN CTTNC 146

(2) INFORMATION FOR SEQ ID :550:

(i) SEQUENCE CHARACTERISTICS:  
10 (A) LENGTH: 221 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :550:

AAATATNGAN TATCCATCCC CTCAAGCATT TATCCTTTGT GTTACAAACA 50  
20 ATCCAATTAT ACTCTTTCAG TTATTTTAAC ATGTACAATT AAATTATTAT 100  
TGACTCTAGT CACCTTGTTG TGCGAGCAAG TACTAGGTCT TATTCATTCT 150  
25 TTCTAACTAT TCCAGGCCCT TTTTAATCAA GAAGGCTCCC TAGACCAAAA 200  
TTTTAAAAAG ACAATGCTAG G 221

(2) INFORMATION FOR SEQ ID :551:

30

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 116 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :551:

40

AAACATCGTT TATTCATCCA GCAGTGTTC TCAGCTCCTA CCTCTGTGCC 50

285

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :547:

ATNCCTTCTC CATCCANTTA GTTANCAGAA ACTAATCAAA AGAAAGTCTG 50  
ACAACTGCAC TCCCCCTTGC ATGCCATTCT CTCAAGCCCA TAATCTTGGA 100  
10 GTATCCACAA CGTGCGAAGG CCTACCCTTT GTGTGTACTC ATCTCACGTT 150  
TACGTATTTT GTNGTTGAGG AGCTCCTCTA CAAATGTTGC GTATCTTCCG 200  
15 AATCACTCAT TTAGAAAA 218

(2) INFORMATION FOR SEQ ID :548:

(i) SEQUENCE CHARACTERISTICS:  
20 (A) LENGTH: 46 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :548:

GGAGGAGACC ATCAGNCCCG TGAAGACCAC TCCTGACGTC TCGTGT 46  
30

(2) INFORMATION FOR SEQ ID :549:

(i) SEQUENCE CHARACTERISTICS:  
35 (A) LENGTH: 146 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :549:

284

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :545:

10	GATTCAGCTC CAGCATCCTT GCCACCTCCC CACCCGGGAG TCAAGGGTCG	50
	TGGTTCTGCC TTGAACAGGC CACAGCCGTA GCTGTAGAGA GGCCAGTGGT	100
	ACATCAGCCC ACCGACAGGA GGAGGAGCCC TGGCTTGAGG GAAGGGGAAG	150
15	CCCAGGCCTG T	161

(2) INFORMATION FOR SEQ ID :546:

(i) SEQUENCE CHARACTERISTICS:

- |    |                            |
|----|----------------------------|
| 20 | (A) LENGTH: 188 base pairs |
|    | (B) TYPE: nucleic acid     |
|    | (C) STRANDEDNESS: double   |
|    | (D) TOPOLOGY: linear       |

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :546:

30	AATAGCCCTG AGGTCATCCT GCAAAGTGCG TATCAAAAAA TACGAAGTTA	50
	GGGTGACAAA GTTTGACAGT GATGTTATAC AAGTCAAAC TGGGAAGGTCA	100
	TAGTAAGCAT ACCTATGCTG AGAGAAAGCA TCAAATCCTT TGTGTACACA	150
35	TTTAGTTTTA TTGTAACAAA GCAACTTGTA CACTTTTA	188

(2) INFORMATION FOR SEQ ID :547:

(i) SEQUENCE CHARACTERISTICS:

- |    |                            |
|----|----------------------------|
| 40 | (A) LENGTH: 218 base pairs |
|    | (B) TYPE: nucleic acid     |
|    | (C) STRANDEDNESS: double   |

283

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 186 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :543:

10

AAGTAGATAG CTTGCATCCT GACACCGTGG CAAAGTTAAG AAAGTTGAAG 50

GAGAAACATA CCTTGAGAGG GGGTTTTCTT TAAACTAGT GTTAGAAGCT 100

15

TAGGGATTTT TTTTTTTATT CCTTACTAAC TTTCACCCAG AACCGCTCTA 150

TTTGACTTGT GCCGACATTG CAAACTTTNT GACAGG 186

## (2) INFORMATION FOR SEQ ID :544:

20

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 153 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID :544:

30

AGCATCCTTG CCACCTCCCC ACCCGGGAGT CAAGGGTCGT GGTTCCTGCCT 50

TGAACAGGCC ACAGCCGTAG CTGTAGAGAG GCCAGTGGTA CATCAGCCCA 100

35

CCGACAGGAG GAGGAGCCCT GGCTTGAGGG AAGGGGAAGC CCAGGCCTGT 150

GCC 153

## (2) INFORMATION FOR SEQ ID :545:

40

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 161 base pairs

282

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 175 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :541:

10

AATTGAATTC TTAAGAAGCT GTCAAATATG GCAGTCTTTT GATGTTAGTA 50  
ATTTTGTTTT CTTCTGTGTT ATTGGTTCAA AGTACTGGCC TTTTCCTTCA 100  
TTTCCAGTAA TTATTTTATA ACTATCACTT TTAATTGAGT GGAAATTAGA 150  
TGATTGTTGTT ATACTGTGAA ACAGC 175

15

## (2) INFORMATION FOR SEQ ID :542:

20

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 221 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID :542:

30

AAGTACCTTT TCCTGCAGCT GCCCGTATGC CTGAGTGACT AAGGGGCAGT 50  
CGTGAGAGGC AGAGTCCAAG ATCTCATTGG TCGTTTCCAG ACTGCCGTCC 100  
AGCCGTGCTG CTTTCATCAGG GCACACTCGC CGCCCTCCTG GGGCCAGGTT 150  
GCACATGTAC AGGTACCCGT CGGCGCACCC ACCAACAACG CGGTCTTCTG 200  
AATCGCGACT GGCNAACAGA T 221

40

## (2) INFORMATION FOR SEQ ID :543:

281

## (2) INFORMATION FOR SEQ ID :539:

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 184 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :539:

AGAAGGTAAG GGAGTGGGAG GCAGGTGGGT GTTCTGGAGG GGGTATCCTT 50  
15 GTGCTCTAAG GGTGCTATGT TCGATGCTGG TGTTCGGGG ATGGTGAATG 100  
CCCTTCTTTA ANNTTAGAGG GAAATCCAAA CCAATAGGCC CCAAGGTTGC 150  
CAGTGGGATA GGGGTGTAAA AAAGTAAATT GGGC 184

20

## (2) INFORMATION FOR SEQ ID :540:

## (i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 154 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :540:

AACTTATAGA AAAGTAAAGG AAACCCCAAC ATGCATGCAC TGCCTTGTGA 50  
35 CCAGGGAAGT CACCCACGG CTATGGGAAA TTAGCCCGAG GCTTANCTTT 100  
CATCATCATG TCTCCAGGG NGTGCTTGCA AAGAGATATT CCGCCAAGCC 150  
AGAT 154

40

## (2) INFORMATION FOR SEQ ID :541:

280

NTCGGCAGTT GTCTTACT

168

## (2) INFORMATION FOR SEQ ID :537:

5

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 147 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :537:

15

CGGATCATTT TTATCTGATT CCAGCCTGCT TGCAACCCTG GAATCCTCTT

50

GTTCCCTGCT GCCTGCCCCCT TGGAAGGNA CAGTGATGTC TTAGGGGAA

100

GGAGGAGCCC CTNTCGGCAG TTGTCTTACT AGGNNNNNTAA TGAAGTA

147

20

## (2) INFORMATION FOR SEQ ID :538:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 250 base pairs

25

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :538:

GTGGAATCTC AATAATGACA CAAGGTACCA ACTGCCAGCA TTTCTGCGAG

50

35

GCAATCCTGC TCTTAATCTG CAAGATGGAC CTTCTGCAG AGAGATTGCT

100

GTGGGTGATT CTAAGGACAG ATTGTTATAT ACGATGTGGG AGAGCAGATT

150

GCTGTTCCCC GCAATGATGA ATGGGCACGG TTTGGCCGAA CACTTGCAGA

200

40

AATNAATGTA AACCNAACT GATGTAGAGA GGACGCAGCT GCCCNAATAC

250

279

TTAG

154

## (2) INFORMATION FOR SEQ ID :535:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 212 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
10 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :535:

15 GATTACCCTA TATCTACAAT TNGAGGTAAA ATAGAAGCAA CACATAAAAG 50  
GGCCTATTTT TGCTACCATG TCATATAATT CTCCATAGTG AATATTGTGA 100  
TAAAGCTACT GAAAACTATG CCTCACAGAG CCTAGCTTCT TGTAGAGCTG 150  
20 GTATTTTACA ACTCGCATTG CTTGGAAATC TCAACACACG TAAGACTCTC 200  
CTAGGAAGGC AC 212

## 25 (2) INFORMATION FOR SEQ ID :536:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 168 base pairs  
(B) TYPE: nucleic acid  
30 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## 35 (xi) SEQUENCE DESCRIPTION: SEQ ID :536:

GGAAGCTCAA TGTCCGGCAG GTCAATGCTT CNCGGACACG GATCATTTTT 50  
ATCTGATTCC AGCCTGCTTG CAACCCTGGA ATCCTCTTGT TCCCTGCTGC 100  
40 CTGCCCCTTG GGAAGGNACA GTGATGTCTT TAGGGGAAGG AGGAGCCCCT 150

278

## (2) INFORMATION FOR SEQ ID :533:

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 287 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :533:

GAAACAAGTT CTCGCTCATC CCTGCATTTT TGCCAACTTC AGCTTGCAAT 50  
15 ATTTATACTC CAGACTATTT TCATCAGACA AAAACCAGTA AGCAGGGTCC 100  
TCTTTGAGAA GAGTTCTCTC TTTGGGAGAC AGGCTGCCTT CGATGACACG 150  
TTTCACAAGC TGGTTGATGG TGCCCACTAC CCGTGATCTG CTCGCTGGGG 200  
20 GACAGCATCA CTCAGACTAC TTGGAGCCTT GCCTGAATTT CAGGTTTCGT 250  
AGGAGGAATA ATTTTCTCCT TCTNTNGTAT CGNCTCT 287

25

## (2) INFORMATION FOR SEQ ID :534:

## (i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 154 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

## (xi) SEQUENCE DESCRIPTION: SEQ ID :534:

AGCCACTGCC CCTCTTGTCT ACGTATTCCC AAAATTAAAC TTTGATGCCT 50  
GACTTTTTGC AGTCAGTTTT AAGTGAGCTC CCTGAGGTGC CAAGGCCATG 100  
40 GTGTCCCCCT GCTGCGTCTG TTCGTCAGCT GAGTTCTTGT GAATCTNTGT 150

277

## (2) INFORMATION FOR SEQ ID :531:

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 204 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :531:

AAAGCATTCA AGTAAGAATA TGGCAATAAA AAACAAAAAT ATCTTCTCAG 50  
15 CATTCAAAAC AAAACGCATA AGTCATTCCT AACTTNAGAG CTTTATAGCA 100  
TTTTCTAGA CAGGAAGGGA AAAACAGTT AGCATTTAAA AGTCCGGAAA 150  
GCTTTTTTCGT TGNNTTAATT ACATCAACNN TCTGCCTTTG TCCAAATCCC 200  
20 TTAT 204

## (2) INFORMATION FOR SEQ ID :532:

25

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 183 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :532:

35 AAAGGAGCTC AGAACTTCAG CTTGAGCAGG AAGAGGAGGA CGTGCCAGAC 50  
CAGGAACAGA GCAGCAGCAT CGAGACCCCA TCAGAGGAGG CGGCCTCTCC 100  
CCACAGCTGA GGGGCTGGGC TAGGGGTGGG TGGAGCCCTT TAAAATACC 150  
40 CTTTCTTCAA AACTTAGCTC TGAATGGAGA AAC 183

276

CTNCGCTGCA AGGTGACTCA CTAAAATCAT NTGTTAACAC CAACATTATT 200

TTTACACCCA GTGTGTAAGC CAGAAGGGC 229

5 (2) INFORMATION FOR SEQ ID :529:

(i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 117 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :529:

ATATTATTCA TCATCCCAAG GTCACATCTA GTAAGATGGA AGACTTGGCA 50

ACAAGTGCAG GTTTTGTGCTT TCTTTGATTC ATATCGTGCA AGACTTCTTC 100

20 CTTAGCCTCT TTGCTTC 117

(2) INFORMATION FOR SEQ ID :530:

25 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 179 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :530:

35 TCGCAGCAGA AGGAAGCTGA TCCACCATCC GGACAACCCG AACCCAAGCT 50

GAAGACGAGA AATGATCCAG AAAGAATGTG CTGCAATCCG GTCATCTTTT 100

AGAGAAGAAG ACAATACACA CCAATGTCGA AATGTGGCAA AATTACTGTA 150

40 TATGCACATG CTGGTGCTAC CCTCTCACT 179

275

GGGAAGC

207

## (2) INFORMATION FOR SEQ ID :527:

5

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 218 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :527:

15

AGCATTCGGT AAGGACGGAC GTGTTCAAGG ACAACTTTGA TGAGATGGAC

50

AGGTCTAGGG AGGTTGTTCA GGAGCTCATT GATGAGTACC ATGCGGCCAC

100

CCAGCCAGAC TACATTTCTT GGGGCACCCA GGAGCAGTGA TTTCCCTCCC

150

20

CACTACTTCT TTNCTTAGAT GGTAACCACA GCCTCGACCA TGCCTGCTCC

200

CTCTGACCCA GCTTCACC

218

25

## (2) INFORMATION FOR SEQ ID :528:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 229 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

35

## (xi) SEQUENCE DESCRIPTION: SEQ ID :528:

AACCTNATGA CTCTCCATCC CTTGAACCA AACATCTAGC ACTCAGCTCC

50

AGCATATTTT ACCATTCAAC CCGAAATTCA CAAACGCTAC TTGTCGACTT

100

40

GTAACCAATT TACTCAGCAA GTGCTGACTC CTTAACGGAT CATCCCCATC

150

274

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 291 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :525:

AAACTGTTCT TTAAAAGGCC TCTCCTGGTT ATTAAGCCAG GAAGAGAAGT 50  
AGAATCTCGA ATCACCTAAN GGAAATGGTG ACACAGGTTG TCCTTTCTCA 100  
GCCGTTGGTT TCCTTTCATC TCTGAAGGCC TGTA GTACCA TGAGGAAAAC 150  
ATTTAATTTA GAGGGTGAAC CCAACAGTAG GAAGCTGAAA GCAGAAGTGT 200  
TTATCTCCCT CTGCATT CAG ACCAGGCTCC TTAGTGCACT CATCAGACTA 250  
TCGCTGCCCC TGCTGTCTGC TGTGAGCCT TCACCACCAC T 291

## (2) INFORMATION FOR SEQ ID :526:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 207 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :526:

CATCCGCGTG CTGGACCCCT TCACCATCAA GCCCCTGGAC AGAAA ACTCA 50  
TTCTCGACAG CGCTCGTGCC ACCAAGGGCA GGATCCTCAC CGTGGAGGAC 100  
CATTATTATG AAGATGGCAT TGGTGAGGCT GTGTCCNNNN GTAGTGGGCG 150  
AGCCTGGCAT CACTGTCACC CACCTGGCAG TTAACCGGGT ACCAAGAAGT 200

273

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 204 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :523:

10

AGTAAGGTTT TGCATCCTTT GATCAGCAGG TAACTGACGA ATTCTTGAGT 50  
CGAAGATTAT ACCTTGATGA GCTTTGATGA GCTCTTGCAA ACGAATGAGA 100  
CCAGTGCTGT CATCATACAC AACCATGACG TTTTCCACTT GAAAAACTGC 150  
ACCAGGTCTA AAATGCACGC TGAGTGAAGA GAAGTCTGGG CAGAGACTGA 200  
CATA 204

20

## (2) INFORMATION FOR SEQ ID :524:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 168 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :524:

ATATCTGTCT CATCATCCCA AGGTTTCACA TCTAGTAAGA TGGAAGACTT 50  
GGCAACAAGT GCAGGTTTTT TGGCTTTCTT TGATTCATAT TGTGCAAGAC 100  
GTTCTTCCCT CAGCCTCTTT GCTTCTTCAC TTNNTCTAAN ATAATCCAAA 150  
GAGGTCAATG TATCATCA 168

40

## (2) INFORMATION FOR SEQ ID :525:

GACTNATAGN TNGACCCACC TGTGA

175

## (2) INFORMATION FOR SEQ ID :521:

5

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 136 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :521:

15

ATGGAATCAA ACAGCTCTAT AATGAAGATA ATGTCTCAGA AAATGTGGGT

50

TCTGTGTGTG GCACTGATTT ATCAAGACAA GAGGGACATG CTTCCCCTTG

100

TCCACCTTTG CAGCCTGTTT CTGTCATGTA GTTCA

136

20

## (2) INFORMATION FOR SEQ ID :522:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 200 base pairs

25

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :522:

AATGGAGCAA TTCATCCAGT TCTTCTAGAA ACAGCTCAGA ATCAAAGCTG

50

35

GATATATTTT GTGTCTTCTG TGA CTGTTCA TTCATGGAAG GAAGCAGACT

100

GCTTTGGGCA GAATTATTCT CCTGACTACT TGAGCTAGTA GACTAGGAAC

150

TATTCCATAA GAGGAAATCC TGTAAGTCTT AAATCCCCAC TGGAGAAAGC

200

40

## (2) INFORMATION FOR SEQ ID :523:

271

AAAGAATATA AAAATCTCGT TCACCCAGTG GTAAGTGTAT TAAATAGAT 200  
CTGTATCATA CACACAGTTT CTCCCGGAGT CGTGAGAATG ACAGGAGGGA 250  
5 CCTGGCAACT 260

## (2) INFORMATION FOR SEQ ID :519:

(i) SEQUENCE CHARACTERISTICS:  
10 (A) LENGTH: 115 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

## (xi) SEQUENCE DESCRIPTION: SEQ ID :519:

AAGCTAATAC AATGGTCATT TCCAGACAAA TTAAAGGAA AACTAAGGC 50  
20 TGCTTCAAAG ATTATCTGAT TCCTTTAAAA TATATGTCTA TATACACAGA 100  
CATGCTCTTT TTTTA 115

## 25 (2) INFORMATION FOR SEQ ID :520:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 175 base pairs  
(B) TYPE: nucleic acid  
30 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## 35 (xi) SEQUENCE DESCRIPTION: SEQ ID :520:

CANGTGGCTT CAATTAAACA ATNAGGAGCC TCNNAACATC CTGTCGCAGA 50  
AACTCCCAAT ATAAACGCCC CCANACACTA ACACAAAACA GCCTTATTAA 100  
40 CCAGATAAGT TCTCCACTAC CACTCCTAGA TTTGATGTAA CCCTGAATNT 150

270

CTCACACTCA TACAAACGCA CATTAAACA CGTGTGNACA NTGTACTCAG 200

ACACACACAG GTGTG 215

5 (2) INFORMATION FOR SEQ ID :517:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 181 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :517:

TCGCAGAGAA GGAACAATCA GGGCCATGAC AGGAACCGCA AAGAACCAGA 50

GGGTATAGGC AGCAAAGAAG GGCACATAAA AAGGCTGCTT CTCAGGAAAG 100

20 TGTCGCACTG AGACAAACAC ACATACAGAC CACACACAGA CCACCACCTC 150

AATCATGGGC CCTAGCCGNC CTNGTAATAC G 181

25 (2) INFORMATION FOR SEQ ID :518:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 260 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :518:

ATGTAECTCA ATCCATCCGC AAGAAAACCA AACCAACAGA AAAGGAAGCT 50

GAAGACATGG ACATCGCAAG CCACGCGGTA ATGCATACTT GGCACAGAGT 100

40 AGCCAATATA GAAGACGTGT GCCTCACACG GTTCACTTTG TTCATCAATA 150

269

CTGNAAGAAA TGACCTGTCT NNTCTNCAGC GCCATTCCCN AACAGATGCC 200

CTAGTCAGGA CCACAACCTCT TAAACCTCAT AGCNAAATAT 240

5 (2) INFORMATION FOR SEQ ID :515:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 183 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :515:

CAATGCCCAA TCTGAGTGTA TACACATCTT AGGAAAAATA ATCTAANGTA 50

ACTTTTGAGG GTGAGAGNGG AAATAAGAGA TCACATTTAT TCAAGACTGA 100

20 TCCCTATNAG GAAGGAGAGG CCCAGGCACA GATACCACAA AAGAGCACAG 150

TACCCAGCTG TCCTGGNATT GNTTGAGTGT AAG 183

25 (2) INFORMATION FOR SEQ ID :516:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 215 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :516:

TCGCAGCAGA AGGAAGTCGT TGACCTGGCA GCCAAGGGAA CACACAAACA 50

CACTCACACA CACATGCACT CACCTGCATA CACACACACT CATAACACCG 100

40 AACACTCATA CACACANGCT TGTGCACACA TGTTTCATGCA CATGCATGCA 150

268

GAGCTTTGTC

210

(2) INFORMATION FOR SEQ ID :513:

- 5 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 222 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :513:

15 CTGTACAATC ATCCTGCAGA AAATTGTTTT GGAGAATTCT TGGTAATTGA 50

AGACCAGCAG AGCACCCCTC CCCACCCGCC CCGTAAAAGT GCTTACAATG 100

AACAGGGATT CTTTTCTTTA CAAAAGACCC AAAGATACGT GGACAAAAAA 150

20 AGAAAAGCTT GAAGTCTCAA TGCCTAATGT GTGCACATAA AACAGGCACG 200

AAGAAACAAA CGTGTGCATC CT 222

25 (2) INFORMATION FOR SEQ ID :514:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 240 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

30

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :514:

GCAGGAGAAG GAAAAGACAG CAACTCATCC CAGAATTGCC NAATGAAGAT 50

GAGGAGAATC CCCTCAAAGG GATCTGTGTG CTTACAGTGG TGACAGTGAC 100

40 AATGAGGAGG ACTGATGAGA GACTCAAGAG TGAGGAAGAG AGCTAGCTGA 150

267

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 255 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :511:

10

ACTGTACCTA TCATCCTGAA AAACCTTATG GGGGAGAAAG GTCAGCAGCT 50  
TCTCTTTCTT TTNATCGAAA ATAATAAAC TCGGTATTCT ACTTTAACTA 100  
AATGTAAGGA AGAAAATATA CAAGCCCATA TTTAATGTAT TTCTATNCGA 150  
GCAACAATAG TTCATATGTT CATGTTTGCT ACTATCACAA TTCAACATAT 200  
GAACACAGAT CAGCTCTATA CCATGAATAC TGCTGGAAGT GATGGTTTAG 250  
GATTA 255

20

## (2) INFORMATION FOR SEQ ID :512:

25

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 210 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :512:

35

GAAAGATTGG ACATGATTGC GTTTATAAGA ATGAGAGTGT TAAATTGGAT 50  
TTCTTGCTTT ATTTGTGACA TTTCAGTTTA TTAGAAATCA TGTTACCATT 100  
AGAAAAATTG AAGTTTCCTA GTAACAAAGT AATTTGATTT GTGTAACCTG 150  
ATAAAAGATT TACTGACTTA AGCTTTTGTT TTTTTCATA AGCTGCTTTT 200

40

266

CCAGCCTTCT CCATGGTGGT GAAGACGCCA

180

## (2) INFORMATION FOR SEQ ID :509:

5

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :509:

15

AAATGCAAAA CTCACCGTGC AACTCCTAG ATCCCTGCCA CAAAGAAATC

50

TTTGAAAAAT GAAGTCTTCC TTTCGGACAA TATACCATN GAGTTTCTCT

100

ATTT

104

20

## (2) INFORMATION FOR SEQ ID :510:

## (i) SEQUENCE CHARACTERISTICS:

25

- (A) LENGTH: 171 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :510:

GTNNATACAC AACTAAGTTC AAATAAAAAA ACCAAATNAA AAATNGGCAG

50

35

GGAAGCTAGA GCCAGAATCA GGAAAATCTG TTTCCTCGTC CCCAGACTCC

100

CGCCAAGCCT ACTCCACTAA CTAACANNGA CTCTATCAAG TTTCTATCAA

150

GACTTGCATC TGNATCTTGN A

171

40

## (2) INFORMATION FOR SEQ ID :511:

265

## (2) INFORMATION FOR SEQ ID :507:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 281 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :507:

CAGGAGAAGG AAGGTTGTAC GTGGACACTA TAAAGGTCAG CAAATTGCAA 50  
AGTAGTCCAG GTTTACAGGA AGAAATATGT TATCTACATC GAACGGGGCA 100  
GCGGGAAAAG GCTAATGGCA CAACTGTCCA CGTAGGCATT CACCCCAGCA 150  
AGTGTTTATC ACTAGGCTAA AACTGACAAA GACCGCAAAA AAACCTTCAA 200  
CNGAAAGCCA AATGTNCCAG CCGGAAAGGA AAGNGCATAC AAGGAAGAAA 250  
CCATTGAGAA GATGCAGGAG TAAAGTATTA T 281

## (2) INFORMATION FOR SEQ ID :508:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 180 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :508:

AGGGNTGCTA ANNTATTGGT GGGCAGGAGG CATCGCTGAT GATCTTGAGG 50  
CTGTTGTCAT ACTTCTCATG GTTCACACCC ATGACGAACA TGAGGCATCA 100  
GCAGAGGGGA CAGAGATGAT GACCCTTTTCG CTCCCCCCTG CAAATGAGCC 150

264

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :505:

10

ACCCTCTTCT GATAAATTTG AGGGCCCGTT TGTCCTTGGA GACCTTCAGT 50  
AACTCCATGG CGCGCCATCG TACGGGGCAA ANACACACCT CCCGAATCAT 100  
GTCCCGCACG AACTTGGTGT GTTGGTCAG ACGCCCGCGT TNGGCNTGTG 150  
CTGGGCTTGC TCACGTTCTT GTCACTTTGT GGCCCTTGTT GAG 193

## (2) INFORMATION FOR SEQ ID :506:

20

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 274 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID :506:

30

ACATGGATAG GCGTATGCAT ACTACGCTAA GGAGAAACAA TGTCCTTACA 50  
TATTACGGGT AGTGAGAACA TTATCTGTAT AACAGGGAAC TGTGATTATT 100  
TAAAAATAGC AGAACTTATT ANCTGTGCTT TAGAAATAAC TGTATACAGT 150  
GTTATAAGTT GAAAAGAACT CAAAATAACT AATAAATATA ACCTATGTAT 200  
TAGAATTAAA AAAGCTGCTT TCTGTGAAGT CAATCAGCTA TATTAAAAAA 250  
TGACACAAAT CCAAACAAGA TGCA 274

40

263

GCTGACCTGG CTCTCGGAAA CGCAGGAGTC TTTCTGAGCC AGCTCAGAAA 150

CC 152

5 (2) INFORMATION FOR SEQ ID :503:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 141 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :503:

CCCTGACCCC TCCTCACCAC CGCGCTGCAC CTCAGGGTTA CAAGAAGAAC 50

TAGGAAATAA CGCCGGCCAC CNGACCCCTG GAGAGGGGCC GGCTAGAACA 100

20 NTTCTAAGAT CCNGCACAGC AGGTCCCGNA TGTNGAACCT T 141

(2) INFORMATION FOR SEQ ID :504:

25 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 107 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :504:

35 CACACGACAC ACGACACGCA CGCAAACACG CCAGACGCGA CAGAGCGCGC 50

GCGGGAGCGG AGCAGCGGAA GCGCAGCAGC GCACACGAGA GATAAGGGCG 100

GCCGAGC 107

40

(2) INFORMATION FOR SEQ ID :505:

262

GTGGAGCTGT

260

## (2) INFORMATION FOR SEQ ID :501:

- 5 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 268 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :501:

15 AAAGGCATAG TAAAAATAAA ATCTACGTAA GTAACAATCT AATACTATAT 50

TAAATNCGTT GCTACAAAGT GTTTTGTTTC TCTAAAAAGT AGTTTTTGCA 100

TATCATTCGA CCTCTTCACC CATNTGCTGG CTTATTGCT TTATATACAA 150

20 CAGTTAAAAT TTGTGCACTA AGCTGAGCTG CCTTCACAAT GTGGTTCAGA 200

CAAAATGCAC CCAAAGAACT ACATGTTAAG AGAGTTTATG TCCATGCTCA 250

25 ACCATGGCTT GCCCAAAT 268

## (2) INFORMATION FOR SEQ ID :502:

- 30 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 152 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

35

## (xi) SEQUENCE DESCRIPTION: SEQ ID :502:

AAAAACTCTA ATCCAGACTA CAGTTGTCGA GATTCAAGTC GTGAGTGCAG 50

40 GAGCGTACAC AGTGCCGTGC TGGCACATGC ACTGCACACG CTCTAGAGAC 100

261

## (2) INFORMATION FOR SEQ ID :499:

## (i) SEQUENCE CHARACTERISTICS:

5

- (A) LENGTH: 195 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :499:

GATNGCCACA TCTCAACACT ATACNACTCG CTNTTCGAAT TCGCCGTNTT	50
AGAACCGCAA GAGACCTTGA TTTAGTCACG CGAGTTCGTC TTCCTGTTCC	100
ACANGAAAAT AAAGCTAGGG AGGTGATTTA TCTATCCGAG AAAAAAGCCG	150
GGGACTGGTG GAANNNGAAC AATGNTCTCT NTGTCGTACT ACAAT	195

20

## (2) INFORMATION FOR SEQ ID :500:

## (i) SEQUENCE CHARACTERISTICS:

25

- (A) LENGTH: 260 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :500:

GCGGCCTTGG GGGCACCGGC GTGTCCTGCC CAGTGGGATT AAAAAATAAT	50
GCTCCCCACA TGGCGGGCCT TTGAGGTTCC AGTAAAAATG CTTTCAACAA	100
ATGGGCAATG CTTGTGTGAT TCACAATCGT GGCATTTAAA GTGCACAAAG	150
TACAAAGGAA TTTATACAGA TTGGTTTACC GAAGTATAAT CTATAGGAGG	200
CGCGATGGCA AGTTGATAAA ATGTGACTTA TCTCCTAATA AGTATGGGGG	250

40

260

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 246 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :497:

10

GAGAGTGGGG TTAGCTCTGC CTAGCGCTAC ACAAGAAAAC CTCCCTCCAG 50  
TAAATNGGTG TGGGNGGTCC GCTTTTGGCC ATCATCGCAC CCCCCGGTC 100  
ACTGGGCGTT GTTGCCGGGC ACTTGTTTNN CNGGCTGGGT GTGTACCGTA 150  
ACCGTGGGTC CTCTGACAAG TGCCTAACTC GGCCACCCC TTAGGGTGTG 200  
TNTCATCGAA GTGTAGNGAA TGGTGAACG TTTGTTTGTN GTGTGC 246

20

## (2) INFORMATION FOR SEQ ID :498:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 215 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :498:

GCCCCTTTAC CAGCAAGTCC TCTACTCAGA AAGAACTGAC CCACGCAAGT 50  
CTGGGAGAGT GACTAGTTCA AATGTGCAGG GCTGAAGCTT CCAAACACAG 100  
CCACTATTTT TGTTGTATAT CTTTCATCTCA ATGGCGACAT GGCCACTGCC 150  
CAAGGAACTT GTGGCAGGGA TCCCAAGGTG AGGCAGCAAC AGATGTCTGT 200  
GAACATCGTG CGTTA 215

40

259

## (2) INFORMATION FOR SEQ ID :495:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 169 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :495:

ACATGACCAT CCGCATCCGC CTTTATTGAC AATGAGAAGA TGGAGTCCCG 50  
GACGCATCTA TCCCTCTTTG GCCCTTACAG GTTTGCCACG AGAGTGAGAC 100  
GCCTTCCTGG ACCAGGGGAG GGNGNGTTGG TNCTNTGNGC GTGNGGGTNT 150  
GTGGGNGCTG CTGGGGAGG 169

## (2) INFORMATION FOR SEQ ID :496:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 172 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :496:

CAGAGAGAAC GTTTCATATGG CTGCTGCTTC TAGGAGTCTC TCGCTCATAG 50  
AAAAGGCACA CACTGAAAGA GGAAGCAGAT CCCATTGCTG TGGAAGTCCC 100  
ATTGTTAGGA AGCTCTGCTT TTCTGGAGTT CAAATTCGCA TTCATGATGC 150  
TTTAAACCGT CAAGCTGGGT GG 172

## (2) INFORMATION FOR SEQ ID :497:

258

CCGTGGGTC

159

## (2) INFORMATION FOR SEQ ID :493:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 197 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :493:

15 GGGCAGAGNA AGAACTGTTC CACCAGGTGA ACAGTCCTAC CTGCTTGGTA 50  
CCATAGTCCC TCAATAAGAT TCAGAGGAAG AAGCTTATGA AACTGAAAAT 100  
CAAATCAAGG TATCGGGAAG AATAATTTCC CCTCGATTCC ACAGGAGGGA 150  
20 AGACCACACA ATATGTNGTG CTGGGGCTCC CCAAGGCCCT GCCACCT 197

## (2) INFORMATION FOR SEQ ID :494:

- 25 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 188 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :494:

35 GATGGGGAAG GGCATCCCAA CACAGCCTGT GGATCCTGGG GCATCTGGAA 50  
GGGCGCACCA TCAGCAGCCT CACCAGCTGT GAGCCTGCTA TCGGGCCTGC 100  
CCCTCCAATA AAAGTGTGAG AACTCCACTG TGTGCCCTGT CTTTGGGCAG 150  
40 GGAGGGCTGC TGTGAGTGGA GTCTTGAGTN GGTGAGTG 188

257

## (2) INFORMATION FOR SEQ ID :491:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 263 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :491:

AGCCAACTAA GTTCTCTCTT CGTGAAACAC AGGTCCATGA GTCGACACAA 50  
ACACTAATGC AAGAACCATC ACGGAAAACC ACCGCAGCAG CTGAAACTTT 100  
TATAGCCCAT AAAAGGACCA AACAAGTAAG CTGAATGACT GTGAAAATAT 150  
GACCTTCCAG AGCGGCACAT AACAGGATAT CAAATCAGGC TGATGCTTAG 200  
CAGGCTTCAA ATATNATGGT CAAATGACTG GATTACTTAN ATGAGGCAAC 250  
TTCATATCGG AAA 263

## (2) INFORMATION FOR SEQ ID :492:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :492:

AGAGTGGGGT TAGCTCTGCC TAGCGCTACA CAAGAAAACC TCCCTCCAGT 50  
AAATNGGTGT GGGNGGTCCG CTTTGGCCA TCATCGCACC CCCCCGGTCA 100  
CTGGGCGTTG TTGCCGGGCA CTTGTTTNNC NGGCTGGGTG TGTACCGTAA 150

256

(xi) SEQUENCE DESCRIPTION: SEQ ID :488:

ACATGGATAG GCGTATGCAT ACTACACTAA GGAGAAACAA TGGTCTACAC 50

5 ANACGTTAGTG AGAACATTAT CTGTATACGG GAACTGTGAT 90

(2) INFORMATION FOR SEQ ID :489:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 99 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :489:

ACCATGAGAC CTACATCCGA ATCTGACCCA GGCAAACATA CCGGGAGCCA 50

20 TACCGCACTA NCGGCTCTTC TCAAATCTCC TGGCCACNCA CCGAGNGCC 99

(2) INFORMATION FOR SEQ ID :490:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 186 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :490:

35 GGAAACCTGG AGGTGCGCAT CCTCGAGTGC GAAGAGAAGG TCTTCCCCAG 50

CCCCCTCTGG ACTCCATGCA CCAAGGTCAT GGCCAGGAGC TCTTGGCAGC 100

TCAGCCCTGC CGCCCCAGAG CATGTGGCGG CTGCTCTCTA CCAGCCGAGA 150

40 GCTTCGGAGA TGCAGCATCT GCGGCGAATG CCCC GA 186

255

## (xi) SEQUENCE DESCRIPTION: SEQ ID :486:

TCGCAAGAGG AGACATTCTG ATCATCCTCA CTGGACGCCA CAGGGGCAAG 50  
5 AGGGTGGTTT TCCTGAAGCA GCTGGCTAGT GGCTTATTAC TTGTGACTGG 100  
ACCTCTGGTC TCAATCGAGT TCCTCTACGA AGAACACACC AGAAATTTGT 150  
CATTGCACTT CAACCATATC GA 172

10

## (2) INFORMATION FOR SEQ ID :487:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 210 base pairs  
15 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID :487:

ATGCTGCACA CTATGTCTCA CAAACTAAAT GGATCCATTA AAAGTTATGA 50  
25 TTTAAAAGGC GACCACCCCC AAAAGAAGTC ATAACACTCA AGGGTGTCAA 100  
TATATACAAC TGTGTAAACA CAACCAATCT ACAACTATAT CAACACAACC 150  
AGCACTCCTC TATGGGCACA GACACACACA CAAAATTGTC CTTGCTTTTC 200  
30 TCAGATATAT 210

## (2) INFORMATION FOR SEQ ID :488:

35 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 90 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

254

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :484:

10 AACATTATCT TGACAACTG AAGAACACTT CAGTTAACAC TACCTCGAAG 50  
AACCATCAAT GACTTGCTTT GAACAGACTA TAAAAGGCAT TCTCAAGGAG 100  
ATTAGAATGT TAATGCCACT TTGATTAGAT CT 132

15 (2) INFORMATION FOR SEQ ID :485:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 129 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :485:

TGTGCGTGGA GACGGTGGAG AGTGGAGCCA TGACCAAGGA CCTGGCGGGC 50  
CGCATTACAG GCCTCAGCAA TGTGAAGCTG AACGAGCACT TCTTGAACCC 100  
30 ACGGACTTCT CGACACCATC AAGAGCGAC 129

(2) INFORMATION FOR SEQ ID :486:

35 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 172 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

253

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :482:

CGGCTCAGNC TGTGGCGCG AAGAGAGTCT AACCCAAAAT TGCAAAACTC	50
CCGTTGATTT CCAGGCCCTA CCACACGGCG ATGTCAACTT GTCCTCCAGA	100
CATGGACGAC TACCAAAGAT CCCAGCTACG AAGCATGGCC TTGCTTAGAA	150
ACNTTTTTAG AT	162

(2) INFORMATION FOR SEQ ID :483:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 250 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :483:

ATATGAAGGA GGAAATGCTC GTCACCTTCG TGAATACCAA GACCTGCTCA	50
ATGTTAAGAT GACCCTTGAC ATGAGATTGC CACCTACAGA AGCTGCTGGA	100
AGGCGAGGAG AGCAGGATTT CTCTGCCTCT TCAAACNT NCCTGAACCT	150
GAGGGAACT TTGGATTCTC CCTCTGGTCG ATACCCACTC AAAAAGGACA	200
CTTTTGATTA GGACGGTTGA AACTAGAGAT GAACGGTTAT CAACGAACT	250

(2) INFORMATION FOR SEQ ID :484:

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 base pairs

252

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :480:

AGATAACGCT CCCATCCCAG GCTAGAGACT CCATCTCTAA TTTNCNCAGT 50  
CCGTCAATGA GAGGCAGGGA CTGAAATCCC AAGTCTGTGTC TCACCGGATA 100  
10 TTTTCCAGGA ATGCCTCTCT TCCAAACATC AGCGACATTT AACAGACCCT 150  
GAGCAGCAAA CTTCTGCCCC AGAGGAAAGC AGAAAACCAA TTTATGTAAA 200  
15 ATTAGAAGCG ATTTGCTTGA TCCATCACTN GCTTCCAC 238

(2) INFORMATION FOR SEQ ID :481:

(i) SEQUENCE CHARACTERISTICS:  
20 (A) LENGTH: 201 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :481:

TCGCAGGAGA AGAAATCAAC CCCTGCTTCT CAAATCCAGA CAGGCCACAC 50  
30 TGGCTAGAAC TTCCACCCAG CAGTCCTGCT CCTGCCCGAA GTCTGCAAGC 100  
AAGTGAACCA CATGTCGCTA TGAAAGCACA CAGACAACAG ATTAGGGCAG 150  
35 ACCTGGCAAA GATATGCCTG TCTGCCATCT TGGCCCCTGT CTGAGGGAGG 200  
C 201

(2) INFORMATION FOR SEQ ID :482:

40

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 162 base pairs

251

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :478:

10	AATCTACCAA CCTTAAAGCT CCCGNGATAA AGCTGTATTT CCAAAAGACC	50
	TGTNTTTATT NGNNGGNGTT NGCTTTCTTT GTCATCTAGA GCCTTGTGT	100
	ACATGCAATG GGTGGGAGAT AGTGGTACCT ACTGTTGNTT CTNTCTGTGT	150
15	NTTCATCATG GTGTTGTCTA GGTCTCCTGA GG	182

## (2) INFORMATION FOR SEQ ID :479:

## (i) SEQUENCE CHARACTERISTICS:

- |    |                            |
|----|----------------------------|
| 20 | (A) LENGTH: 169 base pairs |
|    | (B) TYPE: nucleic acid     |
|    | (C) STRANDEDNESS: double   |
|    | (D) TOPOLOGY: linear       |

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID :479:

30	AAGCCGTCGG GAGCCGCCGC CGCCATCTGA GGGAGGTACC CTGGAAACCA	50
	CCTTTCACGG TGGGGAAGTG CAGTCGCGGT GGGCAGCTCT GGGGCCACGA	100
	AACGGGAGCC TCTAAATCTT GGTCGGGACT GCTCGCCTGG AGCCGCACTC	150
35	TTGAGTCCGA GGCCATCTT	169

## (2) INFORMATION FOR SEQ ID :480:

## (i) SEQUENCE CHARACTERISTICS:

- |    |                            |
|----|----------------------------|
| 40 | (A) LENGTH: 238 base pairs |
|    | (B) TYPE: nucleic acid     |
|    | (C) STRANDEDNESS: double   |

250

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :476:

10 TCTGGGCGGA AGGTGGTGCG GTGAAAGGTG CAGGGACAGA CTGGGTTAGA 50  
GGCCACTCTT GGTCTTATCC TCCATGGCCA CAACAGAGGT GACAAATACA 100  
CGGGTCACTC AGTTACGTTT AGCCACAGCC T 131

15 (2) INFORMATION FOR SEQ ID :477:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 265 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :477:

ACATGGATAG GTGTATGCAT ACTACGGCTA AGGAGAAACA ATGTTCTTAC 50  
ATATATGGGT AGTGAGAACA TTATCTGTAT AACAGGGAAC TGTGATTATT 100  
30 TAAAAATATG CAGAACTTAT TTCATCTGTG CTTTAGAAAT AACTGTATAC 150  
AGTGTTATAA GTTGAAAAGA ACTCAAATA ACTAATACAA ATATACACTA 200  
35 CGTATTAGAA TTCAAAAAG CTGCTTTCTG TGAAGTCAAT CAGCTATATT 250  
AAAAAAGACA CAAAT 265

40 (2) INFORMATION FOR SEQ ID :478:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 182 base pairs

249

## (2) INFORMATION FOR SEQ ID :474:

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 166 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :474:

TNCGTGCCTA GCAAACCTAA ACTCGAACGC ACGTAATAGT GCTCATAATT 50  
15 CTNTNAAGGA CTTTAAACTT TACTCNGTAT GCTNTNTTGA TGA CTCTAGC 100  
AGCCTCGCTA ACCTAGTTTA CCCCACTGTC CCCACCGGCG AACTNTTTGT 150  
GTTAGTACGC GNGTTA 166

20

## (2) INFORMATION FOR SEQ ID :475:

## (i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 109 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :475:

TTTTTTTTTTA GTAACACTAA AGAGCTGTAA AGAACATTGA AGGTGGTCAT 50  
35 TCCTTCAAAA CTGTGTTTTG ACCACACAAG GTGGGCATTA ACAAACAAAT 100  
TCAACTTAA 109

40

## (2) INFORMATION FOR SEQ ID :476:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 base pairs

248

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 262 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :472:

10

TCGCAGGAGA AGGAATGTTT CCAATAGGAA CGCCTGTAGA CTGTTCAGAA	50
GAAATGCCCA AATGAGCCAG ATGAGAAGGC TGAGGGCAGG GCTGCTTTTG	100
GCTCTGAGGA CTATAGATTT ATCCTCTAGG TGATGAGGGA CTATTAACGG	150
CTGGTGAGTC TGGAGAACTG AACAGTGGAA GCTCTATTTT AGATTCACGT	200
GGCAGTAGAG GATAGAGGTG TTTGGAAGCG GTGGGCAGTT GCAAGCTATA	250
TGGGAGACAT TT	262

20

## (2) INFORMATION FOR SEQ ID :473:

25

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 189 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :473:

35

ACAGAAGGAC TTTGTCTCTT TAGCTTGTTT AGCTCAATGA ACATTATCTC	50
GGCAAATGAC TCTGCTTTCT CGAAGGTCCT TCTCCGCTCC AGGTTTACTT	100
GCATCTCTCA TACTTNNTAC AGCCAACATG AACACTCTAT GTATTTTCTA	150
AGCTTTCNTC TGTTCAGAA CTTTGAATTT AAAACGTCT	189

40

247

GTGTGCAGCA CCTACTTCTT NATCGCCGTG AACTGAAATC TAGATTTTAA 250

ACTGAA 256

5 (2) INFORMATION FOR SEQ ID :470:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 109 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :470:

CTCAAAACGA CAATTCTGTG CCTGGGGGAT CTGACCTGGT GAGGTAGCCT 50

20 GAAGTCTGAA TGGAGCCCAT AGTCGAAAAC AACCTAAGAA TCTCTCAGAA 100

GAGGGTTTG 109

(2) INFORMATION FOR SEQ ID :471:

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 139 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :471:

35 GCGGCAGTAT ACAGAAGCCA TATCAGTTGG GAAAAACTTT ATCAATCATA 50

GAGCCTTTTG AAGAAAAATT TGCCAAGCGT GGTTTTTTGC TTGNAGACCT 100

40 ATATATATTA CCTACAGGCT GAGAAAGCTT TGNATTTCT 139

(2) INFORMATION FOR SEQ ID :472:

246

TNATCGAGAN TTTANTCTAG TAANTATATT AATNTNT

87

## (2) INFORMATION FOR SEQ ID :468:

5

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 187 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :468:

15

ACTAGAAGTA CAGCATCCTG CTGCAAAAAT GATTGTAATG GCTTCTCATA

50

TGCAAGAGCA AGAAGCCGAG ATGACACAAA CTTGCCTGG TATTTGTTGG

100

AGCTCTCCTG GAATCACTGA AGAACTTCTG AGGATCGGCC TGTCAGTTTT

150

20

AGAGGTCATA GAAGGTCATG AAATAGCCTG CAGAAAA

187

## (2) INFORMATION FOR SEQ ID :469:

25

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 256 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :469:

35

AGGGCACCAT TACCATCCAT CTGACATCGC ATTTCCATAG AAATGCCAAA

50

GAAAGAAGGT CCTGGGGTTT TTCATAGAAA GCTCAAAAAG TTCAACCTTT

100

GATGCTATCC CCCAGCCCAA TACAAAATAC ACAGAAAAAG CAATTATTAA

150

40

ACATCGGCTT CGTTTCTTTT TCNCCTTTGA ATNTTAATGT TTACATACTA

200

245

CTACCTCTGT GCCAGGGCAG CATTTTCATA TCCAAGATCA ATTCCCTCTC 50  
TCAGCACAGC CTGGGAGGGG GTCATTGTTC TCCTCGTCCA TCAGATCTCA 100  
5 GAGGCTCAGA GACTGCAAGC TGCTTGCCCA AGTCACACAG CTAGTGAAGA 150  
CCAGAG 156

## (2) INFORMATION FOR SEQ ID :466:

10

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 186 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 15 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :466:

20

ACATCCCTGG AAGGAGGGCC TGAGGGCCAG GGAGGGAACA AGGCAGGAGA 50  
CTGCTGGTTC TGGTTTTGGC CACCTACCC TTGGCCACGT CCCCTCCGGC 100  
25 TAAGCCACAG CACAAAGCAG AGCCAGGCTC TGGAGGCCCA GGGCCTCACC 150  
ACTCCCCTNT GTCCCCCAG CAGGGGGACA AAACAG 186

## (2) INFORMATION FOR SEQ ID :467:

30

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 87 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 35 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :467:

40

TNNNGATGAN TATANAAGCA TCATNGACGG TATTCCCNG TCTTGNANTT 50

244

## (xi) SEQUENCE DESCRIPTION: SEQ ID :463:

5      AATTCACTAT GCGTGGCCGC CACAGCTATN CTTGTCCTCC TGGATCCTGA      50  
ACCTTGNAAG CTGCACTAAT GAGTTCAACG GGAGTGCTCT GGGCCCAGGT      100  
GTCAGCTGTA GCAATGCCCC NGCTGCAACT GAAGGNGCCA GCAATGCTA      149

10

## (2) INFORMATION FOR SEQ ID :464:

## (i) SEQUENCE CHARACTERISTICS:

15      (A) LENGTH: 179 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID :464:

ATCATCAGCA GTGTTGCTCA GCTCCTACCT CTGTGCCAGG GCAGCATTTT      50  
25      CATATCCAAG ATCAATTCCC TCTCTCAGCA CAGCCTGGGA GGGGGTCATT      100  
GTTCTCCTCG TCCATCAGAT CTCAGAGGCT CAGAGACTGC AAGCTGCTTG      150  
CCCAAGTCAC ACAGCTAGTG AAGACCAGA      179

30

## (2) INFORMATION FOR SEQ ID :465:

## (i) SEQUENCE CHARACTERISTICS:

35      (A) LENGTH: 156 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

## (xi) SEQUENCE DESCRIPTION: SEQ ID :465:

## (xi) SEQUENCE DESCRIPTION: SEQ ID :461:

5 ACCNTGTTTA ATTANTGCGC GGGCTCGCCG TTTGCATACA ATGGCTTACT 50  
CAGTGCTNNC AGGCTGTGAG TNAATAGAGN GTGTATGACT TAATAAGCAT 100  
TTTATCAGCG TACCTTTTTTC GCCATGCGCT ACCTGCTATT GATGAAGGCG 150  
10 GCTTAGGGCA TCGAAAAACC TAAAAGTCGA GCTT 184

## (2) INFORMATION FOR SEQ ID :462:

## (i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 275 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID :462:

25 AGGAACCNTG TTTAATTANT GCGCGGGCTC GCCGTTTGCA TACAATGGCT 50  
TACTCAGTGC TNNCAGGCTG TGAGTNAATA GAGNGTGTAT GACTTAATAA 100  
GCATTTTATC AGCGTACCTT TTTGCCCATG CGCTACCTGC TATTGATGAA 150  
30 GCGGGCTTAG GGCATCGAAA AACCTAAAAG TCGAGCTTNG NNGTGCCGGN 200  
AACGGCTCTA NANTACTTCT CATTGTAACT AGAGTACCAT ATTCGGCCGT 250  
NNACTGNGTT GTTGCGGACA GATGT 275

35

## (2) INFORMATION FOR SEQ ID :463:

## (i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 149 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

242

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :459:

ACCCATGGCA AATAGGAAGA AGCTCAGTAT CGGCTCCTCC CACCATAACC 50  
CCCACTTCTC CCGCCTCCTG GACCATAGTT TCCTCCACCA TACGGTCCCC 100  
10 CCATGTTCTT GCTACCACCA AAGTTTCCAC TCTCCATTGG ACCGTAGTTA 150  
GAGGT 155

15 (2) INFORMATION FOR SEQ ID :460:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 169 base pairs  
(B) TYPE: nucleic acid  
20 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :460:

TGCTATTTCC CTTTCATAAA GGCACACATT TGATCTTATC TTCTCTTACC 50  
CAACACGCAG TGGCAGTGTG TATTTTCCTT CTCTTTTTTT GTTAAATATT 100  
30 CTGGTTTGTG GAGGTTTACA GACATGTGTT AGTATATCCT TGCCTGCATG 150  
TAGTTGTTCA TTACTAGAC 169

35 (2) INFORMATION FOR SEQ ID :461:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 184 base pairs  
(B) TYPE: nucleic acid  
40 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

241

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :457:

ACACTAACTG	TTCCATCCGT	TATATTTGCT	GTGAGGAAAA	TTAAGATTCC	50	
10	TGTTGTATGG	GCTGCACTGT	TTCTGGAAGA	CTACAGAAAA	TCTAACATGG	100
TTGACACTTC	CTGGTAGCCC	TTCTGTACAT	ACACACACAC	AACCAAGAGA	150	
15	GAAGACAGAG	AGAAAATCCT	GGTCCAAAAG	ATCACATGAC	CTTACTAGTG	200
TTTCCCCAAT	GA CTGTAATT	TATAAACTAA	AAATTG		236	

(2) INFORMATION FOR SEQ ID :458:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 108 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
25 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :458:

30

GAGANNNTT	NNGGNAATG	NTTNCGCACT	GNAGCTAAGA	ANAGNNATGG	50
NNNTAGGGNG	NNAGANGNCN	TGAACAGAGA	AAGCNTGAGG	GCTCTGGGAC	100
35	GCTGGTAT				108

(2) INFORMATION FOR SEQ ID :459:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 155 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

240

(xi) SEQUENCE DESCRIPTION: SEQ ID :455:

TCGCAGAAGG AGGAACGGGG ACTTTCCATC CCCTGAACCA AGGCATGTTA 50  
5 ACACTTGGCT CCAGCATGTT GTCATCATTC AACCAGAAAT CGCACAAATG 100  
CTACTGTGCC GGGGTGNAGC CAATTTTCTT AAGTAAGTGC TGACTIONCTT 150  
AACANNATC TNTNTTNTGG CTGTAGGGTG GCTCAGTGG AATCCATTTTG 200  
10 TTAACACCGA CAATTAGTTG TTTCACACCC AGTGGTAAGC CAGAAGGGCA 250  
TGCTCTNGGG TCTGCCCAT 270

15 (2) INFORMATION FOR SEQ ID :456:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 254 base pairs  
(B) TYPE: nucleic acid  
20 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :456:

TCGCAGGAGA AGGAACCTTG ATGATACCAT TATCCTCACT TAGATGATGC 50  
ACGACCCCTG CGCTGGATAC GGCACGGTT TCTCATTTG CCTTTGCCAG 100  
30 CTCTCATTCG CTGAGGGGCA TAGACCTTTT GATATCATCC AGGCTTTAGT 150  
TTCTTAAGGA GCAAAACAGC TTCCTTGNNC TTCTGTAGC CTTCAACTTA 200  
35 TTAAACTAC CAAGGAAGTT CAGGAAGTTC CTCAANACGA TGACCTTTAG 250  
ACAT 254

40 (2) INFORMATION FOR SEQ ID :457:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 236 base pairs

239

TGGCCATCTC CAGAAAGTTT AACAAAACCC GACCAGGTTG CCCCCTTCAC 100  
TTTCTTACAA CCTCTTCCCC TTCCCCAGGG GCTCTGCTCC TCACTCCAGA 150  
5 TCATCCTTTA GTTTAGAGCT GCGCAGTGAA GTGGATATCA CTGAAGGAGA 200  
TAGGACGCCA GACTACACTG 220

(2) INFORMATION FOR SEQ ID :454:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 275 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :454:

20

GCCATCCTTG ATGGAAAAGA AACTGAAGAG AAAAGACAGC CTGTGGAAGA 50  
AGCTCAAAGG TTCTTTGAAG AAGAAGAGAG AAAATATGAC ATGATATCTT 100  
25 TGCTTTTGAG TTCCTCACGC TCTCTGAATN TTATTGGTTG GACATTCCAT 150  
ATGTAGCATT CTGCTTCAAT ATTATCTATT ATGTGTCTCT CTCTCTTCAA 200  
ATANNTGCCT GTAGGTAAAA GCAAGCTCTG CATATCTGTA CCTCTNGAGA 250  
30 TAGTTTTGCT TTGTCTTTAG CGGTT 275

(2) INFORMATION FOR SEQ ID :455:

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
40 (D) TOPOLOGY: linear

238

CTCCATTAGC TTTATGGGAC ATACGACGCA TAAAGATACT NTCCCGTGCG 50  
NATTTACAC NTGNCAGAGC TATAAACCGG TGNATGATGT GATTTTNCTG 100  
5 TAGAATGATA TGGCCTGATA TGGAGGCCTC TTAATNGGCT TTTTCAAGCA 150  
GCAAAATGGT CTTGNGTGAG TCGTGCCGAG GCTNNNGATC AAAG 194

## (2) INFORMATION FOR SEQ ID :452:

10

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 168 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 15 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :452:

20

ACTTCAAGCT CAACCTATTC TCGTTCTCTT TGTTAGAGGT GTATTGAGGA 50  
TAGCATATTG AGAATATATT CTCTGGTTCA AACCAAAGAT TTTGTGACAT 100  
25 TAAAACTACT TGAATTTCTA CTTCATAATA GGAGTCAGTC ACTTCTGGGA 150  
CTATAGTGAT GCTTGCAA 168

## (2) INFORMATION FOR SEQ ID :453:

30

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 220 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 35 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :453:

40

CGATTCTTGC CCTAGTCAGA GACTATAGCA GCCCCAGAC GTGAACCAAT 50

237

(xi) SEQUENCE DESCRIPTION: SEQ ID :449:

ATATAAAAAA GATCCGCATA ATAAACCAAA TCAGAAAATA ATACCTTGTA 50  
5 ATACCTCTGT AAGAAGCAGA ATACACCATA TGTTATTCAC ATGTATAGGA 100  
GTGATAAGAA AAT 113

(2) INFORMATION FOR SEQ ID :450:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 211 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :450:

20

TAGCATCCAG GGGAAGTTAA TCAATACGCG AAAAATACTG AAATTAAAGA 50  
GACAAGTAGA AGAAAATGAA ATAATCAAGA GATTGAGAAA AGTTGCCAGA 100  
25 AAGCTTGGAG AAAAACCAAG ATATGTAATT TTCGCAGAAG TCAAAGGTAG 150  
AAACTATTTG AGATCAAAGT CCTATAAACA AAGTTAAATG ATTCCAAGAG 200  
GTAAATAGGA G 211

30

(2) INFORMATION FOR SEQ ID :451:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 194 base pairs  
35 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :451:

236

CATGACTGTT TGTTTGCTCT CCTGCCCTAC CACCAAGCAA AGCAGCAGGG 150  
CTCCTGGGGG AGAGGGATTT CAACCCCCCT GATGGCAGGG GTTGCTCTGG 200  
5 GGAGGAGAGA GGAGAGAACA GGCTGTTTTG GAAAATATCC AGCACTTTGA 250  
C 251

## (2) INFORMATION FOR SEQ ID :448:

10

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 253 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
15 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :448:

20

ACACTCCAGA NCATCCCACT AGAAAAACAA TTNNGCAGGA ACGTGATGGC 50  
AACAATCAGC AGCCAATATT CTCAAGAGTT CCTAATCACC AAAAACATAT 100  
25 ACAATNTAGT CTAGAAAAAT AAGTCAATTT CATAAAATAA GTTTTTAGAT 150  
CGAAAAGCAC CCCCTTCACA GGTACAGAGA TACTGAAAAA TAGTCCCTAA 200  
AAATCTACTC ATAGTTTACG GAGAGAAAGG CATGCCATGT GAGTTACGGA 250  
30 GTG 253

## (2) INFORMATION FOR SEQ ID :449:

35

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
40 (D) TOPOLOGY: linear

235

TAGACCACAG GCTAATGGAA TGTCCCGGTC TGNGTCATCA NATTCGTGAA 150  
CCTGNAGCCC CCGCTGAG 168

5 (2) INFORMATION FOR SEQ ID :446:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 243 base pairs  
(B) TYPE: nucleic acid  
10 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :446:

AGGCAGAAGG GACGCTACTG ACTTAAGCCA AACCCCTGATT GGTGGATAAA 50  
GTATTCAGTT GTTCCATTCA TGCCTATCCT TTNTACAGCT CTCGCGACTA 100  
20 TAACAAACAA CTGATAAAAT AGCATCAGTC CCTCCACCAG GTTGCCCTCA 150  
AGGAAGCCAT GTTTGTGACG ATCCGACCAG TCCCTGACGA TCTCTCTAGA 200  
25 CCACCCTGAC CTCGCCGAGA GTGCTGAAGG AGCTATCTAA CCA 243

(2) INFORMATION FOR SEQ ID :447:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 251 base pairs  
30 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :447:

CAGTCAGGGT CACAGAACAG TATTCAAAAT GATTGCCCAC CTGTTTTAGA 50  
40 AATCTAAAT NNTAAGTAAC TAAGAGCAAA GTGCTATGTG GGTTTTAGAC 100

234

CAAGGGGCGG ANGANGACCG TTTNGNTTCC TTGAAANGAG CCCCAGCTNC 150

TCCGNGNGAG ACGCAGTGGA CTNCGATGNT TAGCNCTAGT NNCCCGCT 198

5 (2) INFORMATION FOR SEQ ID :444:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 208 base pairs  
(B) TYPE: nucleic acid  
10 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :444:

ATACTACGCT AGGAGAACAA TGTCCTACA TATTATGGGT AGTGAGACAT 50

TATCTGTATA CAGGGACTGT GATTATTTAA AATATGCAGA ACTTATTTCA 100

20 TCTGTGCTTT AGAAATAACT GTATACAGTG TTATAAGTGA AAGAACTCAA 150

AATAACTAAT ACCAAATATA CACCTATGTA TTAGAATTCA AAAAGCTGCT 200

25 TTCTGTGA 208

(2) INFORMATION FOR SEQ ID :445:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 168 base pairs  
30 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :445:

AGGACATTTC ACTACGGGNT ATGTGCATTC TGGGCTTAGT AATGTCAAAT 50

40 CACTCTTCTC TCCAGCTTGG CCATTCCTCA TTCCTTGCGG GCCTGCCCTG 100

233

ACGTTTCCCC ACACCACCCG AGCTACTTTA CCAGCGATCA TGATTGTGAT 150  
GGAATAGGCT TATTAAGTTA CACATTTAAA AAGTCATTAG AACATCTCGT 200  
5 TCTTGCACAC TAGTGTAGAA AGGTCTTCCA AAGATAAAAG GTGTAGGCCT 250  
GGTT 254

## (2) INFORMATION FOR SEQ ID :442:

10

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 147 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
15 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :442:

20

GGGGNGCTAG CAGTTGGGNG GTGTAGGAGG CATTGCTGAT GATCTTGAGG 50  
CTGTTGTCAT ACTNTTCANG NNNCACACTC ATGACGAACA TGGGGCATAG 100  
25 CAAGGGGCGG ANGANGACCG TTTNGNTTCC TTGAAANGAG CCCCAGC 147

## (2) INFORMATION FOR SEQ ID :443:

30

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 198 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
35 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :443:

40

GGGGNGCTAG CAGTTGGGNG GTGTAGGAGG CATTGCTGAT GATCTTGAGG 50  
CTGTTGTCAT ACTNTTCANG NNNCACACTC ATGACGAACA TGGGGCATAG 100

232

TCGCGTCTGA AATGNTNGTG TGGTAGACCA CCCCCATTCA AGCCTTCATA 200  
CTTCGTAAAA ATGCAAATGT TGAAGATCGN NTCT 234

5 (2) INFORMATION FOR SEQ ID :440:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 203 base pairs  
(B) TYPE: nucleic acid  
10 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :440:

GGACCAGGAA CCTRACTGAG ATAAGTTCAG CTTTCCAGTT GACACCAAGT 50  
CATCTAGTCT TCCCGGAGTA GATATAGTTG AGGTACTCCA TTTCCCAAAA 100  
20 CAGAGAGCTG ATCCCGGGCT GCAACACCTC CAATAGTCGA AGCTCCCTTA 150  
ATNAAGGATA TCAATGTATT TCTTAAACGC TTGATGTCGT TCAAAGTCTG 200  
25 TTC 203

(2) INFORMATION FOR SEQ ID :441:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 254 base pairs  
30 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :441:

GTGATGCACC TGACATCCCC TCACAGGCTC TTGGAGAACT GTAGTGCAAC 50  
40 TCACTTAACC GCAATGCTGA GAGCAGAATT CTGGAGTATG ATCCAGGGGA 100

231

AGGACAACAG TGGCGAAAAA ACAGATACCA AAGGAACCAA ATCAGAACAG 150

CTCAGCAACC CCTGAATTTG 170

5 (2) INFORMATION FOR SEQ ID :438:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 187 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :438:

AGAACTACAG AAACCTGGCC TCCCTGAGTT TATCCTATGG GGGGCACAGG 50

AAAGAGCCCT GGACCATAGA AACCAAGTAC GAGTAGCAAG AAAACCAAAA 100

20 GGGTGGGAAT GGATCAAAGG TGTGAAAACA GATCTGTCTC GTAAGTGTGT 150

AATCAAGGAA CTAGCACCAC AACAGGAAGA TAACCCA 187

25 (2) INFORMATION FOR SEQ ID :439:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 234 base pairs

(B) TYPE: nucleic acid

30 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :439:

AAAAGCAACC AGGTTCGAGA AACAATAGTG TATGTGTTCC TATAGGTATG 50

AGTTATTGAN TGTAGATTCTG TTTTCTGCA ATCCTCTGCC GAAATGATNT 100

40 ACACTTACAA TGNNGAATGC CATAGGACAC TACAATCTGA ATCAAAACAG 150

230

(xi) SEQUENCE DESCRIPTION: SEQ ID :435:

ACACTTGATA CTATGCATCA AAGGACGTGG AGAACTAGAG CGGGCTACAT 50  
5 TAGTATATTT TCGTTGTCAG 70

(2) INFORMATION FOR SEQ ID :436:

(i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 163 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :436:

AGTACGCAAT GCTTTCTTAC AGTAAGCAAG AGCTCCTCTG TAATCCTTCT 50  
20 CGTTGAAGGA AATGCAAGCT TTACCAAGAA GGGCTGGAAT ATTATTCGGA 100  
GACTGATTGA GTACAAAATG AAAGTGTGCG TCAGCTTGAT CCATTTTGTC 150  
25 ACCCTCAAGT AGG 163

(2) INFORMATION FOR SEQ ID :437:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 170 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :437:

TGTGGCTGAT CATAAGAAAG GAGCAAAGAA AGCTAGAATT GAAGAAGATA 50  
40 AGAAGAAACA GAGGACAAAA AACAGACGT TAAGGAAGAA GATAAATCCA 100

229

CCATGNCGGC CCCCAGGTCC TCGATCTTTT CGAGCTGACT TCTCATGGCT 50  
 CGATTTCTTG GTGCTTGGTT TGGTAGCTTC AAGCTGGGAT TCGAGGGTCC 100  
 5 CCGACTNTTC CACCATACAG GACCCATCGA GGAGGCATGT TCTGGTCTNT 150  
 TGGATCCACT GGTGGAAGGG TTGCGCGCTG GNCAAAGTGT TGGTNTAACT 200  
 NGNCGTTTCC TCT 213

10

(2) INFORMATION FOR SEQ ID :434:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 221 base pairs  
 15 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :434:

CCATGNCGGC CCCCAGGTCC TCGATCTTTT CGAGCTGACT TCTCATGGCT 50  
 25 CGATTTCTTG GTGCTTGGTT TGGTAGCTTC AAGCTGGGAT TCGAGGGTCC 100  
 CCGACTNTTC CACCATACAG GACCCATCGA GGAGGCATGT TCTGGTCTNT 150  
 TGGATCCACT GGTGGAAGGG TTGCGCGCTG GNCAAAGTGT TGGTNTAACT 200  
 30 NGNCGTTTCC TCTGCCGGTG T 221

(2) INFORMATION FOR SEQ ID :435:

## 35 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 70 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

40

## (xi) SEQUENCE DESCRIPTION: SEQ ID :431:

AAAGTGGCGCT TGGGCATCCT GCCAGCCTGC CATGTCTTCA TGGCTGGTC 50  
GAAGGCAGCC NGGACTATGG CCAGGAGGCG AATGTAGTCA CTCAGGAGCT 100  
CAGCAAGGAG GAAGAAGTCA TTGTT 125

## 10 (2) INFORMATION FOR SEQ ID :432:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 222 base pairs  
(B) TYPE: nucleic acid  
15 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## 20 (xi) SEQUENCE DESCRIPTION: SEQ ID :432:

GCCTAACTGT CAAAGCACAG AAAAGTTAAC AAAGGGTGGG ACTCGCCATT 50  
TCGAAATAGC ACATTTTGTAG CAATAGGCTC TCTACACTAG AGAGCCAGTA 100  
25 GACTGATATT CTTTAATGCC AGTTTCCTAG TTAATCGTAA AGATAGACAC 150  
AATTCCCCC TTTATAAAG CTTCTGTCGT TTCACATAAT GACTTTAACT 200  
30 ANAANGGAAA TGGGGCAGGA CA 222

## (2) INFORMATION FOR SEQ ID :433:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 base pairs  
35 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

## (xi) SEQUENCE DESCRIPTION: SEQ ID :433:

227

(xi) SEQUENCE DESCRIPTION: SEQ ID :429:

5 GACTCATCTT GCCCAAGAAG AGCCAGGATA TGAGAAGATG GGAGAGGGAA 50  
GGGGAGGTGT GAAACGTGCT GGTGCTTCCT GTCCTCATGG TGTGATGGCT 100  
GCCCAGGCTG CTCCTTCGAG GCAGGACAGG ATTCCCATGG GAGATATGAG 150  
GACCATGGTG ATTTCCAGGA CCAGTTATGT CCAGA 185

(2) INFORMATION FOR SEQ ID :430:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 277 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :430:

GGGATGCCCT GACCTGATGG CCCTTGACCA ACATGGTGCT GGAGGAGCAC 50  
25 TACCTGGTCG TGGGAGTAGT GGTATCGTG GACCCAGGGG TGATCCCTAT 100  
CAACTCTTGG GGTGAGAAGC AGCGCATGCA CCTGCGGGAC GCTTCCTGGC 150  
TGACCAGCTG GACCCCATCT AGTCGCCTAC AACAGCGAGC CAGCACACCG 200  
30 GCCCAGGTGC CGGAGATGAA TGAGCCCCAG CAGTCCAAGG TGTGATGTGG 250  
GAAGACACCG CAGAGCTCAC TTACCAA 277

35 (2) INFORMATION FOR SEQ ID :431:

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 125 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

226

(xi) SEQUENCE DESCRIPTION: SEQ ID :427:

CTCTGTGCCT CGCTGAGGAA AAATAACTAA AATGGCAAAG AAGATCCTAA 50  
5 GAAGCCGAGA GGCAAAATGT CATCATATGC ATTTTNTGGC AAAGTGTGG 100  
GAGGAGCATA AGAAGAAGCA CCAGATGCTT AAGTCAACTN TAAGAGTTTT 150  
CTAAGAGTGC TC 162

10

(2) INFORMATION FOR SEQ ID :428:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 220 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :428:

ATGCAGAAAA GGAGTCGTGA GCGTAACACC CTCGCTGCTG GTCATAAAAC 50  
25 CCATAGTTCC TGAATCATC AAAGAACTTA ACTTCCTGAC GCCAGATATC 100  
TGCCATGCGC GAAGGGNTGA TACCACTCAG GATTATGAAT TTTGTTTAAA 150  
GTCGNGTTTA CAATGATTTG NCCTGGACTG AAATTCANGC TGCCTTAAGG 200  
30 TGCTGATGAT ATTGAGAAGT 220

(2) INFORMATION FOR SEQ ID :429:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 185 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

225

GAGGAGTCAC AGTGGAACCT CCCAGCTTTA AGATATCTAG CAGAACTAT 150  
AGCTGAGGAC TAAGGAATTC TGCAGCTTGC AGATGTTTAA GAAAATAATG 200  
5 GCCAGATTTT TTGGTCCTTC CCAAAGATGT TAAGTGAACC TACAGTTAGC 250  
TAATTAGG 258

## (2) INFORMATION FOR SEQ ID :426:

10

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 275 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 15 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :426:

20

TCCACATCAT CTCAAAGCC CATAGGCCGA GAAATGGCAT CTGAGATCTG 50  
CTGGGCCACC TCCTGTTGTT CCGTATGTCA GTCATCAGTT CATCTACCTN 100  
25 GTCAATGTCC ATGTCCTGGT AGGCCTTCTT CATGCTTTGN CAGCAAGCTC 150  
CATGCACGAA GGA CTTCTGC ATTGGTAGTG GCATTCTCAA TAGCCTCAG 200  
CTGAAACTCC AGGGTGGATA ATGCCCCGTC AATTTGTGCC AGCTGCTGTT 250  
30 CGAATNNTTT TCTTTCTCGT AAAGC 275

## (2) INFORMATION FOR SEQ ID :427:

35

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 40 (D) TOPOLOGY: linear

224

.. TGCTATCCCC CAGCCCAATA CAAAATACAC AAAAAAGCAA TTATCAAAT 150  
ACTGACTTCG GTTCTTTTT CTCTTCAAT NCCTATAATN GCTTTACATA 200  
5 TTCGTATCAG CACCTA 216

## (2) INFORMATION FOR SEQ ID :424:

(i) SEQUENCE CHARACTERISTICS:  
10 (A) LENGTH: 168 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

## (xi) SEQUENCE DESCRIPTION: SEQ ID :424:

CGACGAAGGG AGTACTCGCG CTTGTCTCC CTATCCACAC TTGAGCAAAT 50  
20 GCTCGCTGGT CTACTGCCAA AACCCATTTC ACCAACCATA TGTCCCTCGC 100  
CCATACCCCC TCTCCCTCTC AAACCCTGGG GACAAATTCA AGGACCCAGG 150  
25 GGTGCCCTTT TAAAAAAA 168

## (2) INFORMATION FOR SEQ ID :425:

(i) SEQUENCE CHARACTERISTICS:  
30 (A) LENGTH: 258 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

## (xi) SEQUENCE DESCRIPTION: SEQ ID :425:

TCGCAGGAGA AGGAGTCGCT TACTATGCAT CCAAAGGCTA CCGTGGTTAC 50  
40 TCCTATATGA CATTCCAGAT TTTGATGACT AGCACCCACC CCACAGCTGA 100

223

TGCTGGCTGT CCTATGCCAG CCTCACCCAT GTGGGGACCA CGNAAGGCAC 200

ACTCCCTCAC CCCGGTGCCG GGCCGTGCGA TCCCCCA 237

5 (2) INFORMATION FOR SEQ ID :422:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 202 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :422:

AGGNGTAATA AATACTGCAT CCTTTCCACA ACATAGCAGG AATCTTATAG 50

GGAAATCCAT ATAGTTTCTG AACATGTATT NATATACTAA GTCTATATTG 100

20 TTTCTTTACG AAGTGTAAT AAGTGCTGCA CCATACTGTA AACAAAACCTC 150

GAATATTGAC TAAATAAAAT CAAAAGTTCA TCTTGTAGTC ATGTCTTTCT 200

25 CC 202

(2) INFORMATION FOR SEQ ID :423:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 216 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :423:

GGGACACCAT TACCATCCAT TGACATCGCA TTTCCATAGA AATGCCAAAG 50

40 AAAGAAGTCC TGGGGTTTTT CATAGAAAGC TCAAAAAGTT CAACCTTTGA 100

222

TA

152

## (2) INFORMATION FOR SEQ ID :420:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 218 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :420:

15 CAGCCCTACA CTCGCCCCGCG CCATGGCCTC TGTCTCCGAG CTCGCCTGCA 50  
TCTACTCGGC CCTCATTCTG CACACGATGA GGTGACAGTC ACGAAGGATA 100  
AGATCAATGC CCTCATTAAA GCAGCCGGTG TAAATGTTGA GCCTTTTTTG 150  
20 CCTGGCTTGT TTGCAAAGGC CCTGGCCAAC GTCAACATTG GGAGCCTCAT 200  
CTGCAATGTA GGGGCCGG 218

## 25 (2) INFORMATION FOR SEQ ID :421:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 237 base pairs  
(B) TYPE: nucleic acid  
30 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## 35 (xi) SEQUENCE DESCRIPTION: SEQ ID :421:

GATGCCAATG TTTATCCAC CGGCTGCACA GGCACAACT CCCCCACCA 50  
GGACGACTGT GATGAGGTGG CCCTCCCTGT CAACCCTGGT CCCTGGAGTC 100  
40 CCCAGCACCT GGGGCCCTGA CGGTCTCGAT GTCACAGGCG CTTACTGTGC 150

221

GAGCTACTG

109

(2) INFORMATION FOR SEQ ID :418:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 202 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
10 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :418:

15 GGATGTAAAT TATATGTTGT TTAAATTTTT CCAGCATCTG AAAACCTTAT 50  
CTGCTAGACA ATGCAAGATT CACACAGAGT TATCTGGGAT TCTGATTTTT 100  
TAAATAGTAC ATATCATTAA ACCATTCNTT CTAAANGTAA GAAGAGCAGA 150  
20 AAAAATCTTA TAAGATTATC AGATTTTCCT AATGACACAG AAATGNAAGA 200  
AA 202

25 (2) INFORMATION FOR SEQ ID :419:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 152 base pairs  
(B) TYPE: nucleic acid  
30 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :419:

TAGCAAATGT GGATTACAAG CAAATACAAC AAGTCGTGCC CCTCCAACCC 50  
ACCACAAACT TCTAAACGCC ACTCAGCAGA TGCATAGGAT TCGTTACACG 100  
40 CAACGATTGA AATAAAAATA AAAGCTNCAA ATGCAATACC CANACTAGCC 150

220

GGATGCTAGT NNNCTCCACC CTNCCCACCT GTCATACCTG TGTANTACAC 150  
ACCCACCCGT ATCACGCAGG ACATGAACCA GCACCACTAA GGCCCCGGNG 200  
5 CAGTGTTCTG NNNTTCTTCT CTANCTGTCT GCCCTGAGTC CCGGACC 247

(2) INFORMATION FOR SEQ ID :416:

(i) SEQUENCE CHARACTERISTICS:  
10 (A) LENGTH: 162 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :416:

TCTAGCACAC AGCTGCGCTC ACAAAAACCTG CGCGACTTGT TAGAACTAAT 50  
20 TGAGTGGAGC CTGCAGGTGA GGGGAGGGAG GGGCTGCAGG TCAGGTAAGA 100  
TCTGGAAGAC AACGCACACT TGAAGGGCAG GGGACTCTAA GCAGGGATTT 150  
25 ACATTGAAAG GA 162

(2) INFORMATION FOR SEQ ID :417:

(i) SEQUENCE CHARACTERISTICS:  
30 (A) LENGTH: 109 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :417:

CAGAAGAAGG AGAACTCATG ATTCCAGAGA GCTTTGGGGC TTATTTTAA 50  
40 GTACTTAGCA AAATATTTGT TTTNCGTGAT TTAGCTTGTC ATTAAACNAA 100

219

TGGAAGCAGG AGTGGAGCTG TCAGGAAGGG CGGCTTCCCG GGCAGGCCAA 100  
CACCCACTTC TCCACCATAG TGCACTCCAC GTCATCATCT GATCACAACG 150  
5 TCCTTCTTCA GGATCTTCAC AGCATAGAGC TCATCTGTGC CTTTCGTTCT 200  
GAAAGCATGA CCTTGCCAAA GCTGCCTTTC CCCAGCACCA TTAGGAAGTT 250  
AAAATC 256  
10

## (2) INFORMATION FOR SEQ ID :414:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 87 base pairs  
15 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID :414:

TCGCAAAGA AGNGTACCAT AACTCCTATT TCNAATGGCT GATTGTAGTA 50  
25 GCACTGGAAG TTTATCAAAA CCCAGGTGTA AATATGC 87

## (2) INFORMATION FOR SEQ ID :415:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 247 base pairs  
30 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

## (xi) SEQUENCE DESCRIPTION: SEQ ID :415:

AGAGGGGGAC CAATCTAACC ATCGCTCTTC CAGTCCTACC AGCACACTCT 50  
40 TGCAGCGCCA TNCCACTCCC TGAGCTCAGG ATCCTAGCCC GCCCGCCCGC 100

218

AACGAAGNGT TCCTGAATAC CACAGCCTGC TGGGAAATGA CTAGGCGGTA 50  
AGGTTCTGCC ATGCCTGTGA CCCACCATGG ACATACTGGA CCTTAATTCC 100  
5 TCTGCTTCTG TGCTCCCTCC TGAGAACCCT TTATGAGCCT GATTCCTCAG 150  
TCTCACCAGA ATTCTGGATC ACCCAAGAGG AAAAGACTGC CAGTTCTAGA 200  
TTCCTCTATA GGGAGACCTG GATTGTTGAC CAGGTGAGAA GCCAATGGT 249

10

(2) INFORMATION FOR SEQ ID :412:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 143 base pairs  
15 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID :412:

AGAAGGAGAC AAAACACCTC CTCTGTAATA GTACCTCGAA TGGATTCAGC 50  
25 TTTACTCCTC TATAACTCAT CTTACACCN GCATATTTAA ACAAATAAC 100  
AAAATGAAAT ACTAATAGTA AAAAGGCTGA CCCATGTGGC TTT 143

30

(2) INFORMATION FOR SEQ ID :413:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 256 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
35 (D) TOPOLOGY: linear

40

## (xi) SEQUENCE DESCRIPTION: SEQ ID :413:

GGGTCCCCC ATTCACGTAC TCCATCACAA AGTACAGGCG GTCCATGGTC 50

217

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :409:

GCAGCACAAG AGTCATCCAT GGATACAGTT CCAATCATTA TAACCACTTC 50

TAAACAAGA TCATCTTCTG CAGCACCTGG TTTTAGTTTA TCCTTGA 97

10

(2) INFORMATION FOR SEQ ID :410:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 155 base pairs

15

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :410:

TTTGAGCTCC TGGACCCTTC TTGCCTACA CTGGCCTTCC TCTCGGAGGG 50

25

ACAAGGAAGC TGGCCTCCCT TTA CTCTACC NTTNNTTNTG GTCCAGGGCC 100

AGCTCTTCCG AGGCTCCAGC CTGCTTTTCG CCGGTGTCAT CAGATCATGC 150

TTTGC 155

30

(2) INFORMATION FOR SEQ ID :411:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 249 base pairs

35

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :411:

216

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :407:

	TATTCATCCA GCAGTGTTC TCAGCTCCTA CCTCTGTGCC AGGGCAGCAT	50
10	TTTCATATCT AAGATCAATT CCCTCTTTTA GCACAGCCTG GGGAGGGNGT	100
	CATTGTTCTC CTCGTCCATC AGATCTCAGA GGCTCAGAGA CTGCAAGCTG	150
15	CTTGCCCAAG TCACACAGCT AGTGAAGCCA GAGCAGTTTC	190

(2) INFORMATION FOR SEQ ID :408:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 194 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :408:

	GAAGACATGG CGCCCTAACA CTTGAGACC TGCTGNTAAA TTAAAGCTA	50
30	TTTTTCATTA AACCACCATT TCCTCCACCT ATTGGAGTCA AATATGAAAG	100
	CTGTCGATGA AGCCTGNCTG GCTGCACAAG TTNGACTGNG TCTGAATAAG	150
35	CACTTTCATC ATGGACTAAG AATCCTTGGT GTGGNCNTGA TCTT	194

(2) INFORMATION FOR SEQ ID :409:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

40

215

CCAAATGACT GTAAGCCAGA CTNGAAGCAT GTCAAAAAG

239

## (2) INFORMATION FOR SEQ ID :405:

5

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 189 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :405:

15

GGCTATTATT CTAAGTGAAG TAACTCAGGA ATGGAAAACC AAACGTTGTA

50

TGTTCCTCACT GATCATTGAG AGCTAAGCTA TGAGGACTCA AAGGCATAAG

100

AATGATACAA TAGACTTTGG GACTTGGGAG GAAGAGCGGG AGTGGGGCGA

150

20

GGGATAAAAG ACTACAAATA TGTGCAGTGT TTACTGCTC

189

## (2) INFORMATION FOR SEQ ID :406:

25

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :406:

35

CACCATCCTC CAAGTAAATC CCCCCTTAGG AAAGTAAGGG AAAAGACCCC

50

TTATAGCCCT GAGCTCCCCC TTGGA

75

## (2) INFORMATION FOR SEQ ID :407:

40

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 190 bas pairs

214

CAATTATCTT CTCGACAGCA TATACAGAAT CCCCACATCT GGAACACTTC 150  
TCAGCACCTC CATANNTTGA GCAAATTTAG AAGTGTTTGG ATTTGTTGTA 200  
5 GGCCTGTGAG GCTGAACACT CTCTG 225

(2) INFORMATION FOR SEQ ID :403:

(i) SEQUENCE CHARACTERISTICS:  
10 (A) LENGTH: 95 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :403:

AGAAGGGGCA TACTCGCTGG AGACCTGGTG CCTCTATCCA CTGNACGCTG 50  
20 ACTGNGGCTT CCACTGCGCC CGTGTACNTT ATCGAAGCTA CAGAT 95

(2) INFORMATION FOR SEQ ID :404:

(i) SEQUENCE CHARACTERISTICS:  
25 (A) LENGTH: 239 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :404:

AGGAAAAATT GACATTACTT GTTAGAAGAG CAACTCTGAA AGAAAACAAG 50  
CAAATTCCAA AACAGAAAAG ATTCACAATN NAAAGGTGCA TACATTAAAG 100  
GGCCCACTG TGTAATACTG TGCCAACTTA TGCAGTCTC ATTGTT CAGG 150  
40 ATGAAATGTG AGATTGTAGT TTGAATGCTA TAAGCAGGTT CCAAGATACC 200

213

TACNCTGAGG CAAGGCAAAC AGTCATAGAA CAGTTATTAA ACAATANAAA 200

ATGTGTT 207

5 (2) INFORMATION FOR SEQ ID :401:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 217 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :401:

GAGGCATGGC CACATTCCAA GAAATGGAAT AAGGAGTGGG ACAGCAGGCA 50

20 GGGGGCCAGC CTGGGGCCTG GGCCTTTTAA TCTAAGGACT GGGGAGAACC 100

AAGGGACCTT AGAGGTCCTC CAGTCCTCCC CATATNNAAA GAGGGAGAAC 150

AAGCCTGGAG AGGAGGCTAC CTTAAGACCC TAAGAAGAAT TTAGCAATCG 200

25 NTTCTCCAAA GATAGCC 217

(2) INFORMATION FOR SEQ ID :402:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 225 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :402:

TTTACAATAG ATTTACCTT CANTTTAGTC AGAGTTGTTG ATTCAAGACT 50

40 CTCCCCACAC TCGCACATCG AAACATTTTT GTGCCAGGGC TTTCCAGCTC 100

212

## (2) INFORMATION FOR SEQ ID :399:

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 278 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :399:

TCACCTTGATT CATCCGTCGC GGGATTGGG AGCACTAGCA ACATAATCAA 50  
15 CACACTCCTA CAATCTTAGG CTTACATGT GCTGATGATG ATGAAACCAA 100  
CTCTGCCCCA ATCATCTCCC CTTCTNTTAG GGTCTTACTA CATATCGCAA 150  
CAGAAGATAA TATTGAGGTG AAGAGGGTAA CATGAAGTTT GGCACTACCC 200  
20 TGAAGAACTG TAGGCATCTC TTGGAATGTG CTAAGGAACT TGATGTCCAA 250  
ATAATGAGAT TAAATTTATG TTTCGAGT 278

25

## (2) INFORMATION FOR SEQ ID :400:

## (i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 207 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

## (xi) SEQUENCE DESCRIPTION: SEQ ID :400:

GGCCAAACTC ACAGGAGCCT AGGCACAGAG CACTGAACAC TGGCTCTGCA 50  
GCGGGAAGGA ATTAGAGCCT TCTGCTTTTG CACCTGCTTT GAGTTAGGAA 100  
40 GCAAGCTCTC TTCCTTGCCA GACTTCCCTT TGGGGCAGGA CACTTTTTTA 150

211

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 218 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :397:

10

GGACACATCC ACCCAGTGAA CTGGACTGTG GCCATGACCC AGGGTATCAG 50  
CTCCAAACTC TGCCAGGGCT GAGAGACACA TGAAGGAAGA TGATGGGAGG 100  
AAAAGCCCAG GAGAAGTCCA CCAGGGACCA GCCCAGCCTG TATACTTGCC 150  
ACTTACCACC AGGACTCCTT GNTCTGCTCT GGCAAGAGAC TCTTGTCTGA 200  
ACACTGCTTA TCTGACCC 218

20

## (2) INFORMATION FOR SEQ ID :398:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 250 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :398:

GGAAGCAAAA AAACAAAACCT AAGCTCGAAT TTGCTTCCAA ACCTGTAGAT 50  
TGCATCTAAC CANGTGTCCC TATGCACCTC AGAGTACTGG AATACGAACC 100  
CAGCGAGACC TTGTCCCCTC CCATTTTGCT GNACTTTTGT TGGTGAAAAT 150  
GAGAATGAGT TNATCCCTAC NTACTTAGTT TAATGCATTT GACCCCAGAA 200  
AACCCAGTA CCTTTNNACA ATGACCCAAC CANTACCTAC CATCGGCCAG 250

40

210

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 244 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :395:

10

AAGAGGGGCT AAGACCCAAG TCATCCTCCA CTTTCGTTTT GTTATATTTT 50  
GCTTAGAATT GCCTCTTCTT CTCCACTTCA GAACTGCCTC AAAATTGACC 100  
CCCTTGACTG ATTTATTGTC GTCAAAGCA TGTTCCTCTA TCTTTTNNNN 150  
TCACGATC CGCTGCCTTT CTACATCTGA GAATCTTGTC AAGCATGGAT 200  
AAACTTGNTT TTATGTTGCA TATTTTNACG GCTTCAACTT GAGT 244

20

## (2) INFORMATION FOR SEQ ID :396:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 185 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :396:

TAATATCGCC ATGTAATGGT ATACATTGTA AGGCTTATGT CACTAAAGAT 50  
TTTTATTCTG ATCTTTCCAT AATAAAGGTC ATATGATACT GTATAGACAA 100  
GCTTTGCAGT GAAGTATAGT AGCAATAATT TTCGTACCTG ATCAAGTTTA 150  
TTGCAGCCTT TCTTTTCCGT TTCTTTTNTG AAGGG 185

40

## (2) INFORMATION FOR SEQ ID :397:

209

AAGAAAATTG ACAAATAATA GAGGTCCTCA AGCCCACGGA CTCCTGGTCT 250  
GAGCCCAAT 259

5 (2) INFORMATION FOR SEQ ID :393:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 189 base pairs  
(B) TYPE: nucleic acid  
10 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :393:

AAAGATCATC AGTTTGAAG GTACTGGTCC AATTATCTA GGAAGTATCT 50  
CTTGAGTTT CAGAAATGCT AGCTTGGACA ACTGAAAAGT CACATCACAG 100  
20 CTGGCATTCT GGGGGCTACC AAAACACCCC TCNNGGAGTA GAAGCTGCTG 150  
GAAGGCAGGC CTGAGCCATT CACCACGGAC AGGAAGAGC 189

25 (2) INFORMATION FOR SEQ ID :394:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 97 base pairs  
(B) TYPE: nucleic acid  
30 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :394:

AGAAGGGGAG GTCGAAGAAA TGTGGCTGAT CATAAGAAAG GAGCAAAGAA 50  
AGCTAGAATT GAAGAANNNN GAAAGAAACA GAGGACAAAA AAACAGA 97

40

(2) INFORMATION FOR SEQ ID :395:

208

TTGCCTCACC TGTGGGGCCC CAGCAGGGAG GAGTCACCAG CCTAGAGGGG 150  
CCAGGTATAC ACCTTANAGA GGATGAC 177

5 (2) INFORMATION FOR SEQ ID :391:

(i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 139 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :391:

GCTCCACTTC CCACATAANA CNAGACCTCT CACAAAAGAG TTCACTGATA 50  
TGTGAATGCA GCTTTCTCCC CATGGTAGCC AGGACAGGGT GCACATTAAG 100  
20 GCAACCCCAA AAACACCTCT TNCTGNCTGC CTCTGCAAA 139

(2) INFORMATION FOR SEQ ID :392:

25 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 259 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :392:

35 GAGGAGCTGC CCTCAAGGTC GTGCGTCTGA AGCCTACAAG AAAGTTTGCC 50  
TATCTGGGGC GCCTGGCTCA CGAGGTTGGC TGGAAGTACC AGGCAGTGAC 100  
AGCCACCCTG GAGGAGAAGA GGAAAGAGAA AGCCAAGATC CACTACCGGA 150  
40 AGAAGAAGCA GCTCATGAGG CTACGGAAAC AGGCCGAGAA GAACGCGGAG 200

207

ACCTACTTCT TTATGCCGTG AACTGAAATC TAAGATTTC AACTGAAATC 250

(2) INFORMATION FOR SEQ ID :389:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 268 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :389:

15 GCCATCTCCC CGCCACCCNC TCGTCCCCTT CTTNTCNNGC CACCCTTCCT 50  
CNCTCNTCCG TTTTNGCTCC ACTCCACTCC TCCNTTTTNA GTACCCTCCT 100  
CNTTTATNTA GAGTTACTGA GAGCCGACCT GACGTCTCCA ACATNCCGTN 150  
20 TCTTATATCT CATCNCGGTT NTNGANGAAT GNAGTNAGGG TTTCCGGGAG 200  
AGACCNAACT TGCTCTAGCC CTTTCCAGCC GCTGTTGTTA AACTGACCTC 250  
25 GTAGGGCNTG AGGGAGGT 268

(2) INFORMATION FOR SEQ ID :390:

- 30 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 177 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :390:

40 GTCAGAGGCA GCCCATCCAG CACGTGCTAG GTGTCCCAT ACGCACAGGA 50  
GAGGCGAGCT AGCCAGCCAA GGCGGGCAGG CGGGGAGGCC CTCTAGCTGT 100

GGACGAGGCG T

161

## (2) INFORMATION FOR SEQ ID :387:

- 5 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 170 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :387:

15 GGTGAGCCTC CGCCATCCAG CCAAAC TGTGC CGAC CGCAGCTGTG 50

CCGTGGCACG ATGGCGAGGA AGCCAGCCCC AAGGACAC TGAAAACACA 100

ACCAGTCAAT GCCGTGTGGT TTTGTTTGAA TATAAATNGC TGAAAGTGTT 150

20 GTTTTTTNAG GCAGTAATNT 170

## (2) INFORMATION FOR SEQ ID :388:

- 25 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 250 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :388:

35 TCCATCTGAC ATCGCATTTT CATAGAAATG GCCAAAGAAA GAAGGTCCTG 50

GGGTTTTTCA TAGAAAGCTC AAAAAGTTCA ACCTTTGATG CTATCCCCCA 100

GCCCAATACA AAATACACAG AAAAAGCAAT TATTAAAAAC GGCTTCGGTT 150

40 TCTTTTTTCT CTTTAATNNC CTACAATNGC TTTACATATT CGTGTGCAGC 200

205

CCAACCAACA GTCAAACCCC AGCGTGGTAG CACGAGGTCC AGAACCTCTG 150

CTTAGTGGGC CCGTATAATA AACGCAACCT GACCCAATTN NGGTTTCTTT 200

5 CCCCAT 206

(2) INFORMATION FOR SEQ ID :385:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 134 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :385:

GAATGCTTGG GATCATCCAG GTGNTCTAT TTATAGGCAC CTGTGTTTAC 50

20 CAGCAGTCTC TCTATTAGAA TGCTTGGTGT GCCAATGTTT CTTGAATTAG 100

AAGCCTGGGG NCACCTAGGT GTTTCTATTA TAAA 134

25 (2) INFORMATION FOR SEQ ID :386:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 161 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :386:

CAAGGCCTTC CTGCACTGGT ACACGGCGAG GGCATGGACG AGAGGAGTTC 50

ACCGAGGCCG AGAGCAACAT GAACGACCTG GTGTCCGAGT ACCAGCAGTA 100

40 CCAGGACGCC ACGCCGACGA ACAAGGGGAG TTCNGAGGAG GAGGAGGCCA 150

(xi) SEQUENCE DESCRIPTION: SEQ ID :382:

5 AAGCAGAGTA CGCACGTCAG GCCCTTCCAC GCCCACCCTCA AACTTTTAAA 50  
CNTACTGGGC GATGGGGCCG TTTNGCTGGC AGTTCAAGAT AAAACA 96

(2) INFORMATION FOR SEQ ID :383:

10 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 196 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear  
15

(xi) SEQUENCE DESCRIPTION: SEQ ID :383:

20 GGACTTGATG GCTTCTTTCA AAGTCATAGA CTTGTGGTAA ACTTCTTGCA 50  
AGGAGCTCTG GGCACCCTCT GAAGCAGAGC CAATTGCTCG AGCATCACAC 100  
TGTACAAAGG TCCAGATGGG TTCATATGAA ACAGCTGGAG TCCTTTTCAT 150  
25 CAATNCNAAT NGANNGGTTA CTCCAAAGGG ACGAGACATG CACCTG 196

(2) INFORMATION FOR SEQ ID :384:

30 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 206 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear  
35

(xi) SEQUENCE DESCRIPTION: SEQ ID :384:

40 AAGGAGGCCT TTGAGTCCCA TCCTCTGCCA CGCAGAGAGG CAGGCCTGGC 50  
ATTTACAGCCT CACTTTGTGT AGGTCACTTT TCGGTCTGTG TTGTAGCTCA 100

203

CTGGCTCACC TGGACAACCT CAAGGGCACC TTGCCACAC TGAGTGAGCT 50  
GCACTGTGAC AAGCTGCACG TGGATCCTGA GAACTTCAGG CTCCTGGGCA 100  
5 ACGTGCTGGT CTGTGTGCTG GCCCATCACT TTGGCAAAGA ATTCACCCCA 150  
CCGTGCAGGC TGCCTATCAG AAAGTGGTGG CTGGTGTGGC TAATGCCCTG 200  
GCCCACAAGT ATCACTAAGC TCGCTTTCTT GCTGTTCA 238  
10

(2) INFORMATION FOR SEQ ID :381:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 275 base pairs  
15 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :381:

GTCCTATGGC ATGAATGTTT GCAACCAACC CAGGAAAAGC CTTAAAGGAA 50  
25 ATAGCTGTTC ACATAGGAGA CCGTGACAAT GCTGTACGCA ATGCTGCACT 100  
CAACACCAAG CAACGATGCA CAATGTACAT GAGGATCAGG TGTTCAACT 150  
GATTGGAAAT CTTTTTGAAA AGGATATGAG CATGCTCGAG GAGAGGATTA 200  
30 AGCGTCAGCA AAGAGACCCT CTCTGCACCA ATAAACAGG TGAAGAAAA 250  
CCTAGCNCGC ACAGAACATA AGCTC 275

35 (2) INFORMATION FOR SEQ ID :382:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 96 base pairs  
(B) TYPE: nucleic acid  
40 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

202

GGCAGTGCCT GCTTCATCCC TTTATGAAGA ACAGAAAATT ATGACTACTC 50  
TACAAGGTGG ATAATACTTC GGTACCTTGC TTGCCACAGC CCTGTTCCTC 100  
5 AAAGCTGAAT TGATAAATTT CTCTTTGACT TCCAAGACCT AGCAGTTATA 150  
AGGCGCCTTG AATAAAGTTT GTGCCTGAAA ATGTGGAGCA ATGCT 195

(2) INFORMATION FOR SEQ ID :379:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 210 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :379:

20

GTAGCCCTGA GGTCATCCTG CAAAGNGCGT ATCAAAAAAN ACGAAGTTAG 50  
GGTGACAAAG TTTGACAGTG ATGTTTACAA GTCAAACCTG GAAGGTTATA 100  
25 GTAAGCATAC CTANGCTGAG AGAAAAGCAT CAAANCTNNG GNACATANTN 150  
GGTTNTNGN AACAAAGCAA CTTGTAATTT AAGNTTAAAC NGAGCATCAT 200  
ATANNNNNGG 210

30

(2) INFORMATION FOR SEQ ID :380:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 238 base pairs  
35 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :380:

201

(xi) SEQUENCE DESCRIPTION: SEQ ID :376:

GGGGAATCCC ACCTCACCCA TTGNGGTGAA ATGCTTTTTT CTAAGAGGTG 50  
5 AAATCACTCG CTGGTGTTTA TTTCGGCACA ACCAGAAAAT AGTGNGGGAT 100  
ATTGAATTAT GGGAGGCTCT GACTGTCTCG NGTGCAGCTT ACATTCACAG 150  
ATGGGGGGTA GTTTTTATAT TCTATAAGCG AGCATATTAA ANGCAATATG 200  
10 AGTCAGTCCT GCATTTATGT CTT 223

(2) INFORMATION FOR SEQ ID :377:

15 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 122 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear  
20

(xi) SEQUENCE DESCRIPTION: SEQ ID :377:

25 GGCTCAGGAT CCGGCATCCT TTATGCCTCC ACAGCACCTT GCTCTTCCC 50  
CAGCCAATCA CTTTAGATGC TGAATCGATT TTAAACANAT GTTTTGT CAT 100  
ATGGCTAATC AAGAGCCAGG TA 122  
30

(2) INFORMATION FOR SEQ ID :378:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 195 base pairs  
35 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :378:

200

NCCATTTGGA GCTGAGATGT GTAAGCTGGT GCCTTTAATA CAGAAAGCCT 100  
CCGTGGGAAT CACTGTCTGA GTCTTGTC TAGTATTGAC AGATATAGCT 150  
5 TTGTTCTTGG AGTAGAATTA AGGAATTGCC 180

## (2) INFORMATION FOR SEQ ID :375:

(i) SEQUENCE CHARACTERISTICS:  
10 (A) LENGTH: 323 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

## (xi) SEQUENCE DESCRIPTION: SEQ ID :375:

GGACCATTCT GATCATCCTC ACTGGACGCC ACAGGGGCAA GAGGGTGGTT 50  
20 TTCTGAAGC AGCTGGCTAG TGGCTTATTA CTGTGACTGG ACCTCTGGNC 100  
TCAATCGAGT TCCTCTACGA AGAACACACC AGAAATTTGT CATTGCCACT 150  
25 TCAACCAAAA TNGATATCAG CAATGTAAAA ATCCCAAAC ATCTTACTGA 200  
TGCTTACTTC AAGAAGAAGA AGCTGCGGAA GCCCAGACAC CAGGAAGGTG 250  
AGATCTTCGA CACAGAAAAA GAGAAATATG AGATTACGGA GCAGCCAAGA 300  
30 TTGATCAGAA AGCTGTGGAC TTA 323

## (2) INFORMATION FOR SEQ ID :376:

(i) SEQUENCE CHARACTERISTICS:  
35 (A) LENGTH: 223 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

199

CTCCTAGTTG TTCCACCTTG GCTAACAATT TACCAATCTT TTTTCTATG 100

AACACGTTCT GCCTTTGCTG CTACTTC 127

5 (2) INFORMATION FOR SEQ ID :373:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 257 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :373:

AAGCGCTCAA TTCGCATCCA CAATGCAACC ACGAACTGAT TTTCTCTTTC 50

TTTTTCAGTT CTCCTTGGTC TGTAACAGGA ATGCCCTTA CTCAGTAGCA 100

20 GGCGGACACG GCCATGGGTC AAGACACCCT GCTTCATGGG GAAACCTTGT 150

TTGTCGTTCC CACCACTGAT TCGGACCACA TAACCTTATN NNATCCCGAG 200

25 CGTTAGCAGC AACTTTTGTG GCCATACGCT TCTCATAGAA AGTACGAAGT 250

TTGGCAT 257

(2) INFORMATION FOR SEQ ID :374:

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 180 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :374:

40

GCATCATCAT TGACATCCCT ATCAATGTCT ACGCTGCTGG CAGAGGACTG 50

## (xi) SEQUENCE DESCRIPTION: SEQ ID :370:

5 GAGACTTAAG TAAAACGGCT GCAGGCCAGA TTCGCCCACC AGCTCAGAGA 50  
CCACCTTTAT CCATGCTTTG AAGTAGGACT CCTTCCGTCT TCAAAATNTT 100  
GAAGACCCTA ACANGCTTTT ATGATGGGGG TCATATCTAT GGTCACGNAT 150  
10 ATAGTAGAAA CCAAAGAAT GTAAGTATTT GTNNATGATT TAAAAAT 197

## (2) INFORMATION FOR SEQ ID :371:

## (i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 114 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID :371:

GCATCTGNCA GCTGCTGCAG GCTGACAGCC TCCAGACCTG GACAGAATTC 50  
25 ATAACTCCC GGAGCTGAAA AAACCGAACA TAAGGGAGTG CACAAGAGCC 100  
GGGCTTTGGA GAGG 114

## 30 (2) INFORMATION FOR SEQ ID :372:

## (i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 127 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

## (xi) SEQUENCE DESCRIPTION: SEQ ID :372:

CTTTCTCTAC TCCATCCATT ATCTCCGGGA TTCCTCCACA TTCCCTTCAG 50

197

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :368:

GGTTCCCGCT CTCACAGCCA TTGCAGTACA TGAGCTCCAT AGAGACAGCG 50  
10 CCGGGGCAAG TGAGAGCCGG ACGAGCACTG GCGACTTGTG CCTCGCTGAG 100  
GCAATACTAT AATANGCAAG GAACTTTTGA GGCCGAG 137

15 (2) INFORMATION FOR SEQ ID :369:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 192 base pairs
- (B) TYPE: nucleic acid
- 20 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :369:

GCCATCATAA GTTCAAAGA AAAGAGAAAG TGTTATTTTT CTGTTAGTGA 50  
CATGTAGTCC CTTTGTTCTA GTAGGAAAAA AGGTGCCTAG AGGTAGTATA 100  
30 TAGAGTAAAT ATTGTTTCCTT TGCCTACTCG TGCTTCCAAT GATTAAGGAA 150  
ATGTAAACA NNNGTNAAAG TCTGTTTTGT CAATGCGGGA GT 192

35 (2) INFORMATION FOR SEQ ID :370:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 197 base pairs
- (B) TYPE: nucleic acid
- 40 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

395

## (xi) SEQUENCE DESCRIPTION: SEQ ID :788:

ACAAATAGCG ACCTCCTGGA GAAAAATCGA AAACGGCCAA GTGGATACCT 50  
5 CACGTGGTTC ACGTCTGAAC AACGGCGAAT GTGAGCTACC TCAGAACCAG 100  
TACCCGAAGT TGCTGGAAGG CAACCACATT TGGTTCAAAC GAGGCGTGGA 150  
AGAACCTCAC GACACGCTTA CGGAGTCCAT GAACGCTTGT TGCAATCCAG 200  
10 GAACAATTCC GCGACACCCT TCGTCTGACA AAAACCTTC GTGACGCGTC 250  
GAGTATCCGC 260

## 15 (2) INFORMATION FOR SEQ ID :789:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 208 base pairs  
(B) TYPE: nucleic acid  
20 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## 25 (xi) SEQUENCE DESCRIPTION: SEQ ID :789:

AACCCACCAT GGTGCTGTCT CCTGCCGACA AGACCAACGT CAAGGCCGCC 50  
TGGGGTAAGG TCGGCCTGCG CACTATGCGT GAGTATGATG CAGAGGCCCT 100  
30 GGAGAGGATG TTCCTGTCCT TCCCCACCAC CAAGCCCTAC TTCCCGCACT 150  
TCGACCTGAG CCACGGCTCT GCCGAGGTTA GGGGCCACGA CAAGAAGGTG 200  
35 ATCGACGC 208

## (2) INFORMATION FOR SEQ ID :790:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 289 base pairs  
40 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: doubl

396

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :790:

AAAAGAAGTA	CGGTAAGGCA	AATCCTGAAA	TTAAGAGTTA	CTATGTGCCT	50
GAAAATACAT	TGTTCTACTC	ATTTAGTGTG	ATGGCAATGG	GCGCCGGCGC	100
10 ACTCTTGCTA	TCGACCATCG	TCGCGCTTTG	GATGAACCGT	CGTAAGTCAC	150
AATTAATGTA	GACACAACGT	CGATTCTCGT	GACTTATGGG	GATCGCAACT	200
15 TTCGCGCCAT	TCTCGATCAA	CACAGCCGGT	TGGTCAGTGA	CTGAATTAGG	250
TCGTTATCCA	TGGGTTGTTT	ATGGCTTGAT	GCTAATAGC		289

20 (2) INFORMATION FOR SEQ ID :791:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 232 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
25 (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID :791:

TTTCCTGTGG	AAGTAGTTAA	ATTGATAAAT	TCCAAAAATT	TGGCAATTAA	50
TGCTCATTA	TTAATGGTAG	AGTTTCCATT	AATGAAGTTG	GAAAATACGG	100
35 TGAATCTTTC	AATGAACTCA	GTTAGACATT	CGGAATGAGC	TTCATACATT	150
GTCTTATTAT	CTTTCTTCAA	TTTATCCTCC	AAATCTGGGA	ATTCTGATAA	200
CCAAATTGAA	GCACCTTATC	TATGATCCGG	GC		232

40

(2) INFORMATION FOR SEQ ID :792:

397

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 232 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :792:

10

TTTCAACAAA CAGAAACCAA TTTCCAACCA GAGGGCGATT TCTCCTTGTC 50

TGGTAATATC GAACAAACTA TTTTAAAGAA CTTGATTTCT GGCAACATTA 100

15

AGAGCGCTGT GAAAAATTCT CTAGAGAATG ACTTACTAAC GGAGGCCATG 150

GCGATCGCAT TAGATTCAAA TAACGAAAGA TCAAAGGAAA GTGTCAAGAA 200

TGCCTATTTT GCGAAGTATG GATCTAAATA AC 232

20

## (2) INFORMATION FOR SEQ ID :793:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 292 base pairs

25

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :793:

GGGAACATAT CTTACGGTA GTGANCCCAG TGACCAGATG TCTTATACAA 50

35

GTTCAAGTTA GACAAAACGG GTGTATACAC GTGTTGGTAA CCATTGGCCA 100

ATTCTTTGTC GGTGATGTAA CGTTCAACTT GACGGCGAAG CGATTGCCCC 150

ATTTGGTAAC CAAACTGGCA AACCTGAACC CACTTCTTGA CTCGTAAAGA 200

40

ACAAGTCCAT GTCACGACCA ATCGTCCGGT GGTCACGTTC TTTAGCTTCT 250

398

TCACGACGTG CAATTCTGCT TCAACGTCGG CTTGCTTCCA TT

292

## (2) INFORMATION FOR SEQ ID :794:

5

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 288 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :794:

15

CAGCAGGCAC AACACCATCG GTTGTGCTG AAAGTATTTT TAAGTCTTTG

50

GCCAAGAAGT CAGTTTCAGC TAAGTTAGAC GGCACCTATG CGGGTATGCA

100

TGATGTCATT CCTGCATCCG ATGATTTTTTA ATTAATTACA ACAACTGATG

150

20

ATGAAGCGTC GAATTCGTCG CGTCATTCTG CCTCACACTC ACAGGCACAA

200

GCCTTAAAGC ATTTGCCAAA GTTTGCTAAC ATGCACTTTG GCGCGGCAAC

250

25

CATTTATTGA AAATGGTTTC TACTATGATA CAAATAAC

288

## (2) INFORMATION FOR SEQ ID :795:

30

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 258 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

35

## (xi) SEQUENCE DESCRIPTION: SEQ ID :795:

GTGGCTATGT ATAAGCAGAT ATTATCTAGT AAATGTAAAG TGAACCCAAT

50

40

CGATAGACCC AAAAAGTGTT TTAAGTGGAA AACACCTTAT GAGGTTTATT

100

399

TTGATGAACT GTTGCACTTG GTTTGATAAT TCAAGGCATT AAGGCAATAT 150  
CTCAATCACC GCATTTTCCA CAACCGGCCA CAAAACAGCT CGTCTATTTC 200  
5 GAGGTCAGTT ACGGCGTCCA GTCTTTGAGC AGATGATTG CCCCAGTGA 250  
TCGTCGGC 258

## (2) INFORMATION FOR SEQ ID :796:

10

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
15 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :796:

20

TGCTTCAAAG CCTGGCTTAA CCCGCTTGCC CACCAACTTC AATTATACCT 50  
GCCCCTTTGC CTAACATCTC ACCGACTCGG GCAACCATCG TATCAACACC 100  
25 CGCGACTCGA TCCCCATCGT AAAATGATTC CGAACTAACA TTTAACACAC 150  
AATAGATAAT ACCATCAGCA TAATGCAAGG TTTTACCATC CACGACCCAG 200  
AGGCGATCAA TCGCGACTAA CCGTCGTTGT AATTCAGGAC TAGCGGTACG 250  
30 CTCATGTAAC GCGACAATAT 270

## (2) INFORMATION FOR SEQ ID :797:

35

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 210 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
40 (D) TOPOLOGY: linear

400

## (xi) SEQUENCE DESCRIPTION: SEQ ID :797:

AAATATCGCT GCGTGCAGCT GAGTTACTAG CTGTTGAAAC TTATCGTTAC 50  
5 TTGTGTAGGT TGTCTGAAAC GGTCGCAGTC ACCGGTTAGC TTGATAAGTC 100  
AGGTTTTTCAG CAACTGTCAT CAAGCCATCA CGACCTATAT AAGCCACTGC 150  
AATCGCACTT TACATCATTAG ACCCTTAC TAGAAGTAAC TGGCCATCCT 200  
10 GCCACCGCTT 210

## (2) INFORMATION FOR SEQ ID :798:

15 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 218 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear  
20

## (xi) SEQUENCE DESCRIPTION: SEQ ID :798:

25 ATCATAAGCG CTGGAAGTTG GGGCATTGTA CAGGGACAAC TTCGGCCTTT 50  
GTTAGCCCCA AGAGTCTACA CTCTGCCAAT GGTGCGCTCC ATAGGAAAAA 100  
CCACGGTCCA AGGCAAAAAC TACGAACCTC AGATAACCGC AAAGAGGATA 150  
30 TCAACCAGAG GACGGAAATG TAAGCCTATT TTAGCCCAA TAACGAGACA 200  
AGTAGTTGAG CTAAATGC 218

## 35 (2) INFORMATION FOR SEQ ID :799:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 176 base pairs  
(B) TYPE: nucleic acid  
40 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

401

## (xi) SEQUENCE DESCRIPTION: SEQ ID :799:

5 CCTATCAGAA TCCAATGAGA ACTACAATGG TGTGCCCAGA CGTAGAGCTG 50  
AGAATAGCAT TACCAAATGG AACACGTGC TACAGTCAGG ATTAAAAAGA 100  
ACAATACTAC AAACCAAGTA TATCAGGCTA TTATAGCAAA GGCTGCCATG 150  
10 AACAAATACAA CACTGAATTA CTCGGC 176

## (2) INFORMATION FOR SEQ ID :800:

## (i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 254 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID :800:

GCAATTGCTT AATTTGTTCT TCCTTCTTAG CATTTTGCTG AGAAGCCAAA 50  
25 CGTTGCGCCA ATTCAGAAGA TTCACGCCAG AAGTCGTAGT TACCAACGAA 100  
TGGTGTGATC TTACCAAAGT CAACATCCAA GATGTTGGTT GACACGGCGT 150  
30 TTAGGAAGTG ACGGTCGTGG GATACCACAA TCACTAGGTT CGGGAAATCA 200  
GCCAAGAAAT CTTCTAACCA GTTAATTGTC TGCACATCCA GACCGTTGGT 250  
TCGA 254

35

## (2) INFORMATION FOR SEQ ID :801:

## (i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 203 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :801:

5 ATCCAGGCCC ATACCCATCA ACCCTGAAAC AACGATTGAA TCACCAGCCA 50  
TTTAACCACA CATTGCAACA AACTCACATT GGGTTCCGAG CGGCAGTAAT 100  
AACACAGTCG ATCAAACGCA AAATAGATGG GCAATAAGGT CGATACAAAT 150  
10 AGGCAACCTT ACAATTACCA CGATCTGTAG CTATCGTATA ACCAATGAAA 200  
ATG 203

## 15 (2) INFORMATION FOR SEQ ID :802:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 193 base pairs  
(B) TYPE: nucleic acid  
20 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## 25 (xi) SEQUENCE DESCRIPTION: SEQ ID :802:

GACACAACCTG TGTTCACCTAG CAACCTCAAA CAGACACCAT GGTGCACCTG 50  
ACTCCTGAGG AGAAGTCTGC CGTTACTGCC CTGTGGGCTA GGCGAACGTG 100  
30 GATGAAGTCG ATGGCGAGGC CCTGGGCAGG CTGCTGGCGA TCTACCCTTG 150  
GACCCAGAGG TTCTTTGAGT CCTTTGAGGA TCTGTCAACT TCC 193

## 35 (2) INFORMATION FOR SEQ ID :803:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 290 base pairs  
(B) TYPE: nucleic acid  
40 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

403

## (xi) SEQUENCE DESCRIPTION: SEQ ID :803:

5 AACAAAAGTT GAAAATTTTA AATGGTCTTT TTATGGTTTG CGTGACCTAA 50  
AAAGACAAAG TTTATCCTTG CCTTACTGTA TAGAAATGCG TCGTATCCAC 100  
AATAGCGTAC AGATTTTTTCC GCATTAATCC GTGTTTATAT TAACAGATTC 150  
10 GTTAAGTATC GTTTAAAAAG GGAGAGAGGG GATACCCTCT CTCTAGATAA 200  
ATGGGTCATC ATTTAATCCC AAGAATGATG TCGATAAGTA CTTTCTAAA 250  
CGATAACAAG ACCCCCAGTA GGTAGTATAG CAGTCTTTAA 290

15

## (2) INFORMATION FOR SEQ ID :804:

## (i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 256 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID :804:

AACTTGATGG TCGAGGCCAT CTCCTGGGCC GCCTGACGAT ACCGTGGCTA 50  
30 AACAGGTACT GCTGGGCCGG AAGGTGGTGG TCGTACGCTG TGAAGGCATC 100  
AACATTTCCG GCAATTTCTA CAGAAACAAG TTGAAGTACC TGACTTTCCT 150  
CCGCAAGCGA ATGAACACCA ACCCTTCCCG AGGCCCCTAC CACTTCCGGG 200  
35 CCCCCAGCCG CATATTCCGG CGGACCGTGC GAGGTATGCT GTCCCACAAA 250  
ACAGGG 256

40

## (2) INFORMATION FOR SEQ ID :805:

## (i) SEQUENCE CHARACTERISTICS:

404

- (A) LENGTH: 286 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :805:

10	AGCAACCTCA AACAGACACC ATGGCGCACC TGA	50
	CTCCTGA GGAGAAGTCT	
	GCCGTTACTG CCCCTGTGGG ACCAGACGAA CGCGGATGAA	100
	GTCGGCGGCG	
	AGGCCCTGGG CAGGCTGCTG ACCGATTTAC CCTTGGACCC	150
15	AGAGATTCTT	
	TGAGTCCTTT GAGAATCTGT CCACTTCTGA TGCTGTTATG	200
	GGCAACCCTA	
	AGACGAAGGC TCATGGCAAG AAAGTGTTCTG GTGCCTTTAG	250
	TGATGACCTG	
20	GCTCACCTGG ACGACCTCAA GGGCACCTTT GCACAC	286

## (2) INFORMATION FOR SEQ ID :806:

## (i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 291 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :806:

35	TTCTTCATCA GATTTTACAT CTGCCTGATT AGAATCTTCT	50
	ACACTGGCCT	
	CAGAAGATGA TTGTTCAAAA CTTTTTCTAA GTTGCTGTAA	100
	AAAAACTTCC	
	ACGGACAAAG TAAAATGCAG TTCTTTATCG TTTAGCCAGT	150
	GTACAACAAA	
40	AGGTCCAATC TTCTCTTCAT TTTAATTGAG ACTCAGAGAT	200
	GTAATAGATG	
	GAAGAAGTGA AATGTCTGTG GCTGGGTTGA TGCTGGCTGC	250
	AATATGAAAG	

405

TGGCAAAGTG CATTGCTATG CAGTGGAGTG TTACTGTGGA C

291

## (2) INFORMATION FOR SEQ ID :807:

5

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 276 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :807:

15

AGTTTAATCA GCTGCAATGA AAACAAACGT CTTTATTAG GCAGAATCCA

50

GATGCTCAAG GCCCTTCATA ATATCCCTTA ATTTAGTAGT CGAACTTAGG

100

GAACAAAGGA ACCTTTAACA GAAATAGAAC AACAAGAAAG CGAACTTAGC

150

20

GATACTCGCG GGCCAGGGCA TTAGCCACAC CAACCACCAC TTTACGATAG

200

GCAACCTGCA CTGGAGGGGC GACTTCTCCG CCAAAGCGAC GGGCCAGCAC

250

25

ACAGACCAGC ACGTCGCCCA GGAGCC

276

## (2) INFORMATION FOR SEQ ID :808:

30

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 218 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

## (xi) SEQUENCE DESCRIPTION: SEQ ID :808:

GGCCTGCCAA CAGCATAGGG AAGAATCTCA TTGTTATACA TATTAAGAAT

50

40

CGATTCTAAA TAGACCTTTT TACCAGTCGC TGAACTCTT AAATTAAGTA

100

406

ACATCGCTAG CTAATTTTCG TAATGGCCGA TTAATCTTGA AACGGCGGCG 150  
AAGCTTGTTT TTCACACGTT TCCCTTCAGG TCCTTTGATG AATCATACTG 200  
5 ACGTGATCGC TTATCGTA 218

## (2) INFORMATION FOR SEQ ID :809:

## (i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 276 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

## (xi) SEQUENCE DESCRIPTION: SEQ ID :809:

AGCAACCCAG CGCTCAATGG TGCTAGTGAA CACAGTTGTG TCAGAAACAA 50  
20 CCTCAAACAG ACACCATGGT GCACCTGACT CCTGAGGAGA AGTCTGCCGT 100  
TACTGCCCTG TGGGCAAAGG CGAACGCGGA TGAAGTCGGC GGCGAGGCCC 150  
25 TGGGCAGGCT GCTGGCGATC TACCCTCGGA CCCAGAGGTT CTTTGAGTCC 200  
TTTGGGGATC TGTCCATTAC TGATGCCGTA TGGGCAACCC TAAGGCCAAG 250  
ACTAATGGCA AGCAAGTGCT AGACGC 276

30

## (2) INFORMATION FOR SEQ ID :810:

## (i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 199 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

## (xi) SEQUENCE DESCRIPTION: SEQ ID :810:

407

GACTCCACCT GAACGGGCCC CTTCTGAACC GCCTCTGTGG GAGCAGGCCC 50  
CATCTGAGGA GGGTCCATCT GAGCAGATCC CTTCTCAACA GGTTCCTTCT 100  
5 GAGGAGGCTT ACTGCTTTTC TTA CTGATT TATTTTTCAG AGTTTCTTC 150  
TTCGTACTTT TTTTAACGCA AGTATTTTGC TTTTATTCT CCTCCATTT 199

(2) INFORMATION FOR SEQ ID :811:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 254 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

15

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :811:

20

AAACAGCACA ACCAATGACA GGATGCAAGA ACTGATAGGG CGCCGCAAAA 50  
AAAAAGCGGG CCAAAGATGA AGTAAATAAA CGTAAGGGAG GTACCGAATC 100  
25 TGGGGGGCTT GGCCTAGAGT AAGGGAGAGG AGCTTCAACT ATCTCAATAA 150  
GGGCAAGAAA ACACAAACAA CTCCTTCATT CGTCCAAAAT GCTTCTGAAT 200  
TGCACCACAA TTGACACACA CACACCTCAA AGCAGAATCC GCACTGACCT 250  
30 AAGT 254

(2) INFORMATION FOR SEQ ID :812:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 284 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

40

408

## (xi) SEQUENCE DESCRIPTION: SEQ ID :812:

TTTTTTTTTT AGCAATGAAA ATAAAAGTTT TTTATCAGGC AGACTCCAGA 50  
5 CGCTCAAGGC CTTTCACAAC ACCCCCCAAT TTAGCAATAG ACTTCAGGGA 100  
CCAAAGGACC CTTTAACAGA AATAGAACAA CAAGAAAACA AACTCAAAGA 150  
CACTCGAGGG CCAGGGCCTC ACCACACCAA CCCCCTTC CAAACAGGCA 200  
10 ACCTGCACCG GAGGGGAGAC TTTTCGCCA AAGCGACGGG CCAGCACACA 250  
GACCAACACA TCGCCCAGGA ACCTGAAGTT TTCA 284

## 15 (2) INFORMATION FOR SEQ ID :813:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 279 base pairs  
(B) TYPE: nucleic acid  
20 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## 25 (xi) SEQUENCE DESCRIPTION: SEQ ID :813:

ATACAACAGC AGAAACAGGT ATCCACGCAC AGTCCAGCAA CATTTCTTCT 50  
GGTACAACGC AGCTTCAAAG TTCACATCAA ACGTTACTTT GTCATACCAA 100  
30 GGCAAGGATG CTAACGCGAA GTCAATCACG CGAGTGATGT CATTCAACAC 150  
CGGTCACGGT GCCGATGTGA CAATCAAGAC TGAAGGCGAT GACGAAGAAG 200  
35 CAGCACTGCC CGCCGATAAC CGCAGCGATG CAAAAAAAAG AGCTAGACGA 250  
CTGACGAAAC CTGAGAACCC CGAAGGACT 279

## 40 (2) INFORMATION FOR SEQ ID :814:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 208 base pairs

409

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :814:

10 AACGTGCTGG TCTGTGTGCT GGCCCATCAC TTTGGCAAAG AATTCACCCC 50  
ACCAGTGCAG GCTGCCTATC AGAAAGTGGC GGCTGGCGTG GCAACAGTGA 100  
CTGAGAAGAC CAAAGAGCAA GTGACAAACG CCGAAGGAGC AGTGGCGACG 150  
15 GGCGTGACAG CAGTAGCCCA GAAGACAGCG GAGGGAGCAG GGGGCATCGC 200  
AGCAGCCA 208

(2) INFORMATION FOR SEQ ID :815:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 192 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
25 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :815:

30

AAACCACGCT CAGTCAGGTT CCGGCAGCAG CTGCAGCATC TCATCTTCTG 50  
CGACTCTCGG TGCCCTCTCC TTCCGATTTC CGGAAACATG GCCTCCGATG 100  
35 TGGCTGTCTC TGACGACGTC ATCAAGGTGT TCAACGACAT GAAGGCGCAC 150  
AAGTCTTCAA CGCCAGAGGA GGTGAAGAGG CGCAAGCAGA TA 192

(2) INFORMATION FOR SEQ ID :816:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 264 base pairs

410

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :816:

10 GAGAGAACCC ACCATGGAGC TGTCTCCTGC CGACAAGACC AACGTCAAGG 50  
CCGCCTGGGG TAAGGTAGGC GCGACAATG GCGAGTATGG TCGCAGAGGC 100  
CCTGGAAAGG ATGCTCCTGT CCTTCCCCAC CATGTGAGAC CTACTCCACA 150  
15 CACTTCGACC TGAGCCACGC CTCTGCCAGG TTAAGGGCCA CGGCAAGAAG 200  
GTGCCCCGACG CGCTGACCAA CGCCGTGCGC ACGTGGACGA CATGCCCAAC 250  
GCGCTGTCCC CCTG 264

20

(2) INFORMATION FOR SEQ ID :817:

(i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 202 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :817:

ACCCTACACA CATCCGTTCA ACTGTCCCAT CACCCACTTA CACTCCAAAA 50  
35 AAAACCACTC AACAAGCAAA CAACCCATCC TGTTTTTATA ACGTTATCGT 100  
AAC AAAG CCGACCATAA TCAACTTGAA TTTACTTCAC CACAAGGCAA 150  
AGCGATTATT TAGATGAGGC ACTCGCACTA CTGCTTGAAG TGCTACTAGA 200  
40 TG 202

411

## (2) INFORMATION FOR SEQ ID :818:

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 179 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :818:

AGTAGAAAAT AAGTTCAAAA TTTTAGAAAT ACTGGCTTTA TACTCGCCCA 50  
15 TGTATTTACA TTCACAGAGA TCTTTATTTA TTTACAAGCG CTTTGAGTTA 100  
CTGTATAGTT TTTTTTAACA AAAAAGCGTG GGGGGCTCCC TTTAGCATTC 150  
CCCATAGGAT AGGTAATGAA CTTTTTGTT 179

20

## (2) INFORMATION FOR SEQ ID :819:

## (i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 260 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :819:

TGTGCTCTTA TGCTAGATTT ACGGACAGAT TTTCTTCTGC CCTGTAAACT 50  
35 AATAGCATAG GAGCATTTTT TAATACGATT CGATACAAAA AAGAATTTAA 100  
GCAATCTCTC GCCGAGACGC ACAATCAAGA CCATTCATAT ACTGATCTAT 150  
CCGCTGAATA CGAACCTTCA ATCGACTCAA TCCGTAAGTG GATCAAGTTG 200  
40 TACGCGGGTC CACGAAGTGA CAGACGAAAA ATGAACGCAA GCTGATGTAA 250

412

ACGCATCACA

260

(2) INFORMATION FOR SEQ ID :820:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 226 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
10 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :820:

15 ACTCGGCACT TTCTTAGAAT AGACAATTTG CAAAATGTCC ATCCCAGGTT 50  
CATCCTTGTA GCCTAATGTT TCCGTCACCG TTGCCACTAG TTAACGTGGG 100  
TGAACCTTTAT CTGGGAAACG GGTAACATCC GCGACCACAA CTAGACCATC 150  
20 ATTTGACGTA ATGCCATCAG CACTCACCAA AACTTGGCCA ACCAACAGCC 200  
TTTCCGTAAC TGAGTTTGAT TTCTCC 226

25 (2) INFORMATION FOR SEQ ID :821:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 197 base pairs  
(B) TYPE: nucleic acid  
30 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :821:

CACCTACATA TAGATGCACG AAGTACTTGC TCACTTTTTT TGGTTGTAAA 50  
TTTTCAAAGC GTTGAAGGCA GCATTCTTAG CGGCACGGAT GTCCTTATCA 100  
40 GTGAATGAAT CAGGCTTTTC CATGGCCAAC CAACCAACGA TTCGCATCGC 150

413

GTGATTTTCGA ATCATGTCAA GCAAAGCACC GGCTGTATCA TAGTAAC

197

## (2) INFORMATION FOR SEQ ID :822:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 304 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :822:

15 GGACTGGGTG CAGTGGCTCA CACCTCACGT TACATTTTAT AGCTAGCAGG 50  
GTAATGGGGA GTTATGGCAC TCAGGTCACA TTCTAGGGAA TGTTTATCGG 100  
GCAATCTCAA TGGCACCGCA AGCTAAATGA CTTCCAGTGT TTCTCATCTT 150  
20 TCGCCTTTCT TCATCGCAAC CTTTGCCCAA GACATCTGTT TTTTCTGGAT 200  
CACCCCTTGA CAGCCACTGA GGAATGATCT TCTGAAAGTG AATCTTCAGT 250  
25 AGACACATCG CCACACCATC TANGTCAGCC ATCACATGCC CAGGTCTNGA 300  
CATG 304

## (2) INFORMATION FOR SEQ ID :823:

30

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 197 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

## (xi) SEQUENCE DESCRIPTION: SEQ ID :823:

40

GGCCCAGCAG ANGGAGGAAC ACTACCGAGG CTCCAGCTTA ACGGTATTTG

50

414

GAGGTCAGCA CGGTGCTCAC AGAAGCCAGG AACTTGCCCA GGGAGGCGTG 100  
CACCAANGGG GCGAACTCNC GGGGAGGCGG GCGACCAGGG TCACCAGCAG 150  
5 GCAGTGCTTA GGAGCTGGGA GCCGACCGAG CCCACCGAAC TCGCGCG 197

## (2) INFORMATION FOR SEQ ID :824:

10 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 281 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear  
15

## (xi) SEQUENCE DESCRIPTION: SEQ ID :824:

20 AAAACAATG TCATTTTGTA CAGACAAAAT TTAGCAGACT CAAGCTTCCA 50  
CAGTTAGTGC GAGAGCCTGT GGATGGCATA GTTACATAAG AGTCTGTTGT 100  
GGATTCAAAT GTCACCTCTT CCAGGCAGTC TTTCCTGACT TACCCTGGCA 150  
25 GCTTTGTGTT CCCACATTAC TAGTAATGTT TTTTCCTTA ATAGCAATGA 200  
TTTCACTGTA ATAATGTATT TATATGCCTC TCTCCCCCAG ACAGCAAGCG 250  
30 TTTTCCCACA GGTCTCGACA CACAGAAGAT A 281

## (2) INFORMATION FOR SEQ ID :825:

35 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 312 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear  
40

## (xi) SEQUENCE DESCRIPTION: SEQ ID :825:

415

TATTAAATTT ACTAGAATGT TACAGTTACA AATTTGGTAA TGTTCTTTCT 50  
GAAAAACAGC CTAATTTTGC AGCCTGAAAC TTGACTGAAA ATCTCAATAC 100  
5 TTTTATTCAT GATAGAAAAA TAATTCCTGG CTTCATCTCA CAATTA ACTA 150  
ATAATTATGT TAATATAAAA TATAACTGTG CCCTTTCTTT TCAGTGATGA 200  
TCAAAGTGAT TCTCCCAGGC CAAAAATCA AATAAGAAGT TATATTTTAA 250  
10 AAAGACATAA CAAGCCATTC TACCCAGTGG GCATCTTCAG TGTACTCCCT 300  
CTACTAATTG GC 312

15 (2) INFORMATION FOR SEQ ID :826:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 189 base pairs  
(B) TYPE: nucleic acid  
20 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :826:

ACACCAAACA CGGGGAGTGG GGAGTAGAGG CTCTGGAGGT CAGGATGGCA 50  
GGGCAGGGAG GGGAAGGAAG GAGTTGTTGG TCTCACAGTG TGCCTGCCAA 100  
30 TCCCAAAGCC CTAGAGACCC CTTCACTGCA GCACCTGCCC CCGGGTCTCA 150  
GGCAGCTTCA GGGCCAGAGA GCTGCCAAGG GCAAGCAAA 189

35 (2) INFORMATION FOR SEQ ID :827:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 232 base pairs  
(B) TYPE: nucleic acid  
40 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :827:

5 CTCTTAAGGG CTTGAAAATT TCTGTGGGAG TAGGACAGAG TGTAGAACGT 50  
ACAGTAAAAG GCAATAAAAC AGTGGGAATA ATTTTACCAG CTATGAGTAA 100  
AGGAGTAATG GGTATTTACT GCCTGTCATT AATCCACACA TATATCCATT 150  
10 TTAGAGATTA TTTTGTTGCC TGGAAATCTG TCTCATCACA GAGTGTTAAT 200  
ATACACCGGC GGGATATTCA AGAGTGGCTA AG 232

## (2) INFORMATION FOR SEQ ID :828:

15

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 282 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
20 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :828:

25

GGACATTGGA ACACTATACT CTATTATTGC GGTCGTGCCT AGCAGTCTCG 50  
CGCATGTCTC CTCAGCGCGC ACAGTCTCTC TCAGAGAGCT CTTCTCTCTT 100  
30 TATATGCGCA GACCCGCAGA CTGGGAGACC CAGACCCAGG GCAAACCTCTC 150  
TTCTTAGGTA TATCGCACCC ATCATATCTC ACACATCGTG TATGTCGTAT 200  
CATCAGACCC CCATAGAGCA TATATGCTAA ATTAATGCTC TCTTTCATCA 250  
35 GTAATTACCC CATATCATAA AATGCGGGCG GG 282

## (2) INFORMATION FOR SEQ ID :829:

40

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 230 base pairs  
(B) TYPE: nucleic acid

417

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :829:

	CACTACATCC GCAAGTACAA CCGCTTCGAG AAGCGCCACA AGAACATGTC	50
10	TGTACACCTG TCCCCCTGCT TCAGGGACGT CCAGATCGGT GACATCGTCA	100
	AGTGGGCGAG TGCCAACCTC TGAGCAAGAC AGTGCGCTTC AACGTGCTCA	150
	AGGTCACCAA GGCTGCCGGC ACCAAGAAGC AGTTCCAGAA GTTCTGAGGC	200
15	TGGACATCGG CCCGCTCCCC ACAATGAAAT	230

(2) INFORMATION FOR SEQ ID :830:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 226 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :830:

30	TTCCGCAAAT AAAAGAATTC ACTAAGGTAC CAAAACAGAA AATATACAGA	50
	GATCAATGAC TTTCATATAC ATTAACAAAC AAAAGTTCAG AGATAAAATG	100
	GAAGAGAAAT GCTGTTTTTA ACAGTATAAT TAAGATAAAA TATGAAGGTA	150
35	TAAACTTAAC AAGAAATGTT GCAAAACCAT TATGTGAAAA TTACAACACT	200
	CCTGAAGACG CAGACACACC TAACAA	226

40

(2) INFORMATION FOR SEQ ID :831:

(i) SEQUENCE CHARACTERISTICS:

418

- (A) LENGTH: 247 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :831:

10	AGAAGTCCTT CCAAGAGTCT TGGGTATGCA ACAGCCATGG AGGCTGTGAC	50
	CTTTTTCCTT CTTTCTACA GCCTGCAGTT CATTTAAGGA TCACCGGAGA	100
	TGACTCGTGC TCTAGTTCTT AAAATCAAAC AAGGATCTGC CAAATCCAAG	150
15	ACCCTGAATT TGGCCCAAAT TTGTAGAAAC ATTGCTTTTT ACCACCCGGT	200
	GCACCAAAAA TACCTCCCAT TTCAAGGCAA CAACCGCTTT AATTGCT	247

## 20 (2) INFORMATION FOR SEQ ID :832:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 base pairs
- (B) TYPE: nucleic acid
- 25 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## 30 (xi) SEQUENCE DESCRIPTION: SEQ ID :832:

	CACCAGGCAG GGGATCCCGG AGGGAAGCCC TCTGCCAGGG ACATGGTGAG	50
	GGCGTGGCCA TCACCCACGA AGGGAGCATA AATAACACTG GCAGGTGGGT	100
35	GGGCAGCAGG AG	112

## (2) INFORMATION FOR SEQ ID :833:

## 40 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 173 base pairs
- (B) TYPE: nucleic acid

419

- (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :833:

AGCCATTCCC	ACTAGAGGCC	AAACCGCCTG	CCCACAGAGA	TTGACAGCCA	50
ATGTTTATCT	CATAACTCTC	CTCCCAGCAG	TGCACCAGTA	AACTCAGATG	100
CCTGAGTGCT	TGTGGCCACC	ACACAACAGA	TGCGGCCTTC	CTCTTCACTG	150
GCCCCTCGGC	TGCTGCTGGG	TCC			173

15

(2) INFORMATION FOR SEQ ID :834:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 288 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :834:

TGGCCCATGG	GAGCCCTTAT	GAGCAAGTTT	CCAGGTCCTT	ATGACACAAT	50
TCCATCATTC	TCGGGTACA	TCCTTACTCT	CTGGCACAGT	AGAGATGTTC	100
CAGACTTATC	TTATATTTTC	ACTTCCCCAT	ACCTGGAATC	AATCACTTCT	150
CCGAGGATGC	TTGATTCCTT	TTAGTGAAGA	ACAGTCTTTG	GAAACCAACC	200
GTCTAGGGAC	ATCAAGTATG	TTTGCCGCTA	TTGGAGTGTC	ATTGCTCCTG	250
AACCTTCTAA	GTGGACACAG	CTAGGAAATG	TATGTGCT		288

35

40

(2) INFORMATION FOR SEQ ID :835:

(i) SEQUENCE CHARACTERISTICS:

420

- (A) LENGTH: 310 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :835:

10	CTTTTCTATT TTCCTTAAGT GTCTGCCAGT CTGAGAAATA AAGGGACAGA	50
	GTACAAAAGA GAGAAATTTT AAAGCTGGGT GTCCGGGGGA GACATCACAT	100
	GTCGGCAGGT TCCGTGATGC CCCACAAGCC ACAAACCAG CAAGTTTTTA	150
15	TTAGTGATTT TAAAGGGGA GGGAGTGAC GAATAGGGTG CGGGTCACAG	200
	AGATAACGTG CTCACAAGA TAATAGAATA TCACAAGGCA AATGGAGGCA	250
20	GAACGAGATC ACAGGACCAC AGAACTGGGA CCAAATAAAG ATTGCTAAGA	300
	ACGTCTAGGG	310

## (2) INFORMATION FOR SEQ ID :836:

25

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :836:

35

	TCAGTGGAGG AATTAAACT GGTGAGAAG GGGAGGTCAG GTTATCAGTT	50
	GAAATGCCAA GGTTATCTCT AATCTTAGCT AGATTCTGCC AAAGTTCACA	100
40	GAGGTAATCA AAAACTTGAG CATGTATTTA AGGATCCATG ATTGAATTTA	150
	CATCTCCCAA AATGCCTAGC ATTCTTC	177

421

## (2) INFORMATION FOR SEQ ID :837:

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 135 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :837:

CCGTTGCACT TGGTGTGGC ATTCTGCAGG GCGGCACTCT CCCACTCTTC 50  
15 CCGGCCTCGA GCCAACCTGA CGGCAGCCAG ATGGCAGTCG TAGTGCACAA 100  
TGTTGAAGTG GGACACGGTG CTGTAGCCCT GCTGT 135

## (2) INFORMATION FOR SEQ ID :838:

20

## (i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 201 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :838:

30

TCAGTGGAGG AATTAAACT GGTGGAGAAG GGGAGGTCAG GTTATCAGTT 50  
GAAATGCCAA GGTTATCTCT AATCTTAGCT AGATTCTGCC AAAGTTCACA 100  
35 GAGGTAATCA AAAACTCGAG CATGTATTTT AGGATCCATG ATTGAATTTA 150  
CATCTCCCAA AACGCCTAGC ATTCTTCGCC ACATTACAGT AGCAACATCA 200  
G 201

40

## (2) INFORMATION FOR SEQ ID :839:

422

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 181 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :839:

10 TTCTTTGGAG TACATCCTTA CTTTCTGCAC AACAGATGAG AGATGTTCCA 50  
GAACTTATAC TGTATCATAT ATTTTACCTC CCCCCCTATA CACCCTGAGA 100  
15 TATACATATA CACTATCTCC GCTAGAGAGA TGTCTATGAC ATATCACTTT 150  
CTGAGATGTA CACGAACGAG ATCTTTTGAG A 181

## (2) INFORMATION FOR SEQ ID :840:

20

## (i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 222 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :840:

30

CATACAAATG ATTAGAAAGC AATACAGCCT TATTGCTGAT ATGGAGAAGG 50  
TTTTAGTGAA CATTGAGAGG AGTTTGGAAG AAAGTCGCTG CACAATCTTC 100  
35 ATGGATGACT TTGAGGGATT CAAGACTTCA GTGGAAGAAC TAACTGCATA 150  
TGTGAGTAGA AATGGCAGGA GAACTAGAGT TCGAAGTAGG AGCTGGAAGA 200  
TAATAACATG GGTTTAAAAA AC 222

40

## (2) INFORMATION FOR SEQ ID :841:

423

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 293 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :841:

10

CGCTCAGCTG GTCTATCCTG CTCTTCCTCT TGTCCCTGCT CTTGCTGCGG 50  
CTCCTATCTA CCGGCTACCT GCTGCCCGCT TTGCTCCTGC TACCGGCTCC 100  
15 GACTCTGGCG GAGGCTCTTC TCCTGGCTCC TGCCCCTGCT CACAACTCCC 150  
TCGCTTCTCC TCCTCCACTC TCCTCTCCCG ACTCCTGCTC CGACTTTTGC 200  
TCTTACTTTT ATGCCTGCTA GGACTCCGGC TCTTGGGTTT CCCGAACATT 250  
20 GTCATTGTTT TGGAATTCTT CCTTCAGCTT GGTCTTTTGC CGG 293

## (2) INFORMATION FOR SEQ ID :842:

25

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 239 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :842:

35

ATGAGGAGGT GAGGAAAAGG AGAAGTGCAG CTACCATCGA GTGATTCTTC 50  
TGGGATAGGT GTCTCATTTA AATCTCATAA TCATCTTTTT TGGCAGGTCA 100  
GTCAACTTCA GGCTCACAGA TGACAGACAG TTGGCCCCAA GACACACAGG 150  
40 AAATACATAA GTGACAACGG AATACAAGTC CATGAATTAA AAAACCATGC 200

424

TTTTCTCTCC TTGCCACACA GCTTTAGTTT GAAAAAAAAA

239

(2) INFORMATION FOR SEQ ID :843:

5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 154 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :843:

15

TTCCGAATTA TTGAATCTTC TTCTGTAACA TCACAATCTT CCTGGTTTTTC

50

AGAATAAACG CTCTTCTCGC TCGCCTCTCT CTGCACTCAC TCCCACCTCA

100

CTCACTCACT CTATAATAAA ATGTTTGCAC TCAATTTATA TAGTAGTGTT

150

20

TGTC

154

(2) INFORMATION FOR SEQ ID :844:

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 392 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :844:

35

GTCTTTAATT GAGAAAGCTG GAGTGGAGAC CCGATCCCCT GGGAGCAGTG

50

CCAGGAGTTG GGTGGAGACT GAGTGGGGTT TGTGTGGGTG AGGGGGCATC

100

TACTCCTCTT GCAACAAGCC AGAAGTAGAA CAGCCTAAGG AAAAGTGACC

150

40

TGCCTTGGAG CCTTAGTCCC TCCCTTAGGG CCCCCTCAGC CTACCCTATC

200

425

CAAGTCTGAG GCTATGGAAG TCTCCCTCCT AGTTCCTAG CAGGTTCCCC 250  
ATCTTTTCCA GGCTGCCCCCT AGCACTCCAC GTTTTCTGA AAAAATCTAG 300  
5 ACAGGCCCTT TTTGGGTACC TAAAACCCAG CTGAGGTTGT GAGCTGTAAG 350  
GTAAAGCAAG TTCTATCCAA TTAGAAGCTG TTGGGGGCGT AT 392

## (2) INFORMATION FOR SEQ ID :845:

10

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 200 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 15 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :845:

20

CAAAGAATAA ATAATTTTTC TATTCCTGAA AGTTAACTAA TTATTTATTA 50  
GAAAGTCAGA AATATGTGGA AAGCAAAGGA ATATTGAGA AAGTGATATG 100  
25 AAATTAATAA GTGGTAAAAA ATTAATAAAA TTAATATTAG AGTTTCCTTT 150  
GAGCTAATCC TTTATTTATT TATTTTTTTC CTTGAGACAA TGTCTTGCCA 200

## (2) INFORMATION FOR SEQ ID :846:

30

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 311 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 35 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :846:

40

TTAAAAATAC TCTGGAAAGA GCACTTCCAT CGTTCATTTA CATCATATTA 50

.426

	GAAATGGATT TCCGAGTCAG CACTGGCTTC CTCCAGAATA GCAGTCCTGG	100
	AGGAGCGAGA TCTCCCAAG CCTCCAGGAT TGCAGTCTGT TGTGTCCTT	150
5	CACTCCCTAA TAGGTTTGCC TTATTAAAG GACCCACCTT CAGAGCTGCC	200
	AAGGACTTTC TCAGAGCAGC TCCTTGGTCC CTCCGACAGC CTGGGATGGC	250
	ATTTATTCTG GGGCCTGGGT GTGGGGAGGT CCTCACCAGC CTAGGAGTAA	300
10	GAGGAGGTGG T	311

(2) INFORMATION FOR SEQ ID :847:

15	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 287 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
20	(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :847:

25	CAGATCAAGA CTGGTGCCCC TTGCCGATCT GAGCGCTTGG CCAAGTACAA	50
	CTCAGCTCCT CAGAATTGAA GAGGAGCTGG GCAGCAAGGC TAAGTTTGCC	100
	GGCAGGAACT TCAGAAACCC CTTGGCCGGG TAAGCTGTGG GCAGGCAAGC	150
30	CCTTCGGTCA CCTGTTGGCT ACACAGACCC CTCCCCTCGT GTCAGCTCAG	200
	GCAGCTCGAG GCCCCGACC AACACTTGCA GGGGTCCCTG CTAGTTAGCG	250
35	CCCCACCGCC GTGGAGTTCG TACCGCTTCC TTAGTCT	287

(2) INFORMATION FOR SEQ ID :848:

40	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 263 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double

427

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :848:

	GATTACAGGT GTGAGCCACC GTGCCTGGCC TATTAATATG CTCTTAAAC	50
	TCATCCATAC GTTTTCATAG CAAGAAAGCT TATTTCTCCC AACTACCGAA	100
10	TAATATTCTA TCGTATGGCC GCACCTCTGT TTATCCATTT ACCTATCGAG	150
	AGGCATCTTG ATTACTTCTA GCTTTGGATT ATTACAAATA AAACATATACA	200
15	AACACGCAAA CAGAGTTTCT CGTGTGAATA TAAACCCGCA AACCGGCTGG	250
	AGGCATATNA CCA	263

(2) INFORMATION FOR SEQ ID :849:

20

(i) SEQUENCE CHARACTERISTICS:

	(A) LENGTH: 279 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
25	(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :849:

30

	TTGTCAGTCA GAATAGGATG TAAAAGACTA TTTCAAAGAG TTAAATTATT	50
	TGTTAATATC AGAGATCAGC CACAGACAAG AAGTTTATGG ATGAGTGCAG	100
35	CAGTGGTCCA TTGGACATGT TAAATACTCG TGGATATCCA CAATTCGAAT	150
	TGACATTAAA AACGAATGGA TACCCAACTC TGAATTCCAT ATCGTTTTTTT	200
	AATATCAAAA ACACAATTTT AACTACTGAT AAACCAGGCA ACCACCGCAA	250
40	GTTTATCGAA ATCCTGCCGC TACTAAACA	279

428

## (2) INFORMATION FOR SEQ ID :850:

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 173 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :850:

GCTGAAAGTT GAAGTGGAGA GCTTGAAACG AGAACTCCAG GACAAGAAAC 50  
15 AGCATCTGGA TAAACATGG GCTGATGTGG AGAATCTAAA CAGTCAGAAT 100  
GAAGCTGAGC TCCGACGCCA GTTCGAGGAG CGACAGCAGG AGACGGAGCA 150  
TGTTTATGAG CTCTCGACAG AAT 173

20

## (2) INFORMATION FOR SEQ ID :851:

## (i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 240 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :851:

TCGAGAAAGT TTCAATGTGA TTAGATTAAA ATTAAAAGAA TCCATAAAAA 50  
35 TGGAACAAAG AAGAAGAGGA ATGAAATTAC TTTTACTTTA AACAGCATTG 100  
TTATCACATA AAACACGTAT CTTACAAATT CATGGGATAG CCCATAAATG 150  
GGACTACAGC AACAATGGTA GGAGAGTCCA TCCTTCTTCA AAAGCAACCC 200  
40 AGCAGGAATT TTCTGTAAA AATATTTTGT CCGTAATACT 240

429

## (2) INFORMATION FOR SEQ ID :852:

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 314 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :852:

ACTGGACTGG TCAAGAACAA AGCTCATGGC AATAGTCTTT TGAATGTTA 50  
15 AAGGAATTTT TCTAGTTGGC TTTCTGGAGG GCCAAAGAAC AACACATCT 100  
GCTTATTATG AAAGTGTTTT GAGAAAGCCA AAGCTTTAGC AGAAAAACAC 150  
CTGGGAAAGC TTCATTAGAG AGTCCTTCCC CATCACAACG CTTCTGCTTA 200  
20 TTCCTCTTAT AAAACAAGGG CAATTTTGTG AGAGCTACTG ACGATTTTCC 250  
CCTCGAAATT TACTATTTCT ACAGCTTATT AATCTCAAAT AGTAAGCATG 300  
25 TCCTTGCCGT CACT 314

## (2) INFORMATION FOR SEQ ID :853:

## (i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 267 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

## (xi) SEQUENCE DESCRIPTION: SEQ ID :853:

TCCTGAAATA CTCTCTACTG TCACTGCTTC AGTTTAATTT ATAGATAGCA 50  
40 CCAGATATGA GTCCTTATTA GTTCTGATAA CTCTGAAATG GTTATTTGGT 100

430

ATTTCTTCAG TGACAAGCAA ACTATCCCC CACATGCCTT TAATGGCCAG 150  
TGTTTTTCGAT TTGTATACCA ATAAGCAATC TAGGTAGAGG TAATCATATA 200  
5 CTGATACGCT AACCTTTGAA ACATAATTTC CAATCTAGTA AGCTAAAATC 250  
GCGCCAATAC TGCTTAA 267

## (2) INFORMATION FOR SEQ ID :854:

10

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 186 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 15 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :854:

20

GCAGTGGATC TTTCTTTTTT TCCAAAGGAA ATTCATATA GAGTCCATTC 50  
ATAGGAAACA GATAAAATGT GAACGGCTGC AACTGAGATG GGGGAGAGTG 100  
25 GCTTGGAGCC CCCAGCCTCT TTGCTTCTC TTATCCCTAT AGGATGGCCA 150  
TTAGGTGAAG CAGTTTAGCT TGTTGGTTCA GACCTG 186

## (2) INFORMATION FOR SEQ ID :855:

30

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 35 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :855:

40

ATTTTGAAAA GAAACCTACA AAAATTGTAT TTCCATATT CATAGTCAGC 50

431

CAAAAATATT GGTCAACTCA TGCTCTCTGC AAGGTTCTGC AAAAATTGCG 100  
GAGTGGTATA GACAAGGCAC CATTGCAATA TATAATACTT TTTGGGTATT 150  
5 GGCCCAAAAA TT 162

## (2) INFORMATION FOR SEQ ID :856:

## (i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 286 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

## (xi) SEQUENCE DESCRIPTION: SEQ ID :856:

TCTGTGGCCA CAGATGCATA TTACAAGCCC ATCCAGAGCC ATTATGAAGA 50  
20 GAAAGTGGCA ATTTTATTCT CAGCCTGAGA AATCCACACC AATCTAGTCT 100  
GGGTTTCCAA GGATCTGCCG TTTAAGTCAC TTAGCCTCTA TCCTTTCCGG 150  
25 GAACAACCTG CCCCTAGAGA GGGTGAACGA GAATCGTCCC CAGTGCCTCC 200  
AACATAACAA ACCCAATCGC CCTGTAACT TTAAATCTTC AACTCGAGAA 250  
AAAGGCTCAT GACTACTTCT AACCATGCCC AAACCC 286

30

## (2) INFORMATION FOR SEQ ID :857:

## (i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 280 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

## (xi) SEQUENCE DESCRIPTION: SEQ ID :857:

432

AACATATATGG TATTATTTCA CGCTGTACCC AGTCCATTGC TTGAACTTAC 50  
GGGTACCTAA TGAAACGTGG AGGTCCGGAT GTATGAAAAT CTCCTCTTTT 100  
5 CCCCTTTACT TACAGCCTCT GTAGGCAATA ATTATAGAGT AGTATAGATG 150  
ATTTTTCTTT TTTATAAATC TGCCTATCTC CAGGAGGATG GGGCGCGCAC 200  
TTTTAGAAAT GCATATAAAT GCTCTACGCT CCTTTTTTCT GTTACTTAAT 250  
10 CGGCGCCAAG GCCTTTACAT GAATACTCAG 280

(2) INFORMATION FOR SEQ ID :858:

15 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 310 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear  
20

(xi) SEQUENCE DESCRIPTION: SEQ ID :858:

25 CACTGGTTTT CATGACTGAT TTCTTTATTT TTAGTAGTTC TGACATGTTG 50  
GCCAGGCTGG TCTTGAAGTC CCAGCCAACC TCAAAGTGCT GGGATTACAG 100  
CTGTGAGCAC CAGCCCAACC TCGCCTCTTT AAAAAGAAA AACACAAGTC 150  
30 CACTCTGAAG TCAGCCTCTG TAACCTCCCC ACAAGAAAAC CGTTTTACAT 200  
CAGTCACTAA CCAAACAACC AACAGTGCTT CAACACAGAA AGTAAAGCAT 250  
35 TATACAGGGC TTGAACTGTC TTTTAAGCAA GCCCCAAATC CTTTGAAAGG 300  
AGGCAGTAAC 310

(2) INFORMATION FOR SEQ ID :859:

40 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 158 base pairs

433

- (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :859:

10	TCTGTGTGGA GGGGAGGGAC CCAGTCTGGA CCCAGGTGTC ATCATCTCAG	50
	CCACAGCAGG GCCCTCTCAG GCTGGGAAAC TTCTGCCAGA GCTGGCGAGT	100
	CCTCTGCAGG TCAAGCCAGG GCTTGGACAC AACTACTTCA TCTATCGCGC	150
15	AGGAAGAG	158

(2) INFORMATION FOR SEQ ID :860:

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 263 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :860:

30	TTTCTAATAA GAACATAAAA TAAAGGCTAA TTAAAAGAAG GTGACTGAGT	50
	CCAGGAAGGC ACTAATCAAA GATGATATAC AGCCAGGTAA AAAAGAACAA	100
	TTCACAGGCA CAAGACTATA TAACCATCGT TTTATTTTCA AACGTTATAC	150
35	AAAATATACT CTACCGAACT ATAATAGATC ATTAATAGTG GCACAATCTT	200
	TAGATTCGGA ATAACTTGAA AATAAATCCC AACCACGTAA CTTACTAAAG	250
	GAATAATGAG CCA	263

40

(2) INFORMATION FOR SEQ ID :861:

434

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 254 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :861:

10 ATTTGTCTGA AAAATATATT TCTACACGAT CTGATAAAGT TCAGATAAGG 50  
GGCATTCTAT TCCTAAGAAT GTCCTAAAAA TGGAAAACTG ATAAAAGATT 100  
15 ATGCTTAGAA TTATACAGGT AAAAGACCTA CAACAATTGT TCTCTTGTTT 150  
TGATCCCATATA GGTCATTTGT TATTACTCTT CTTCAACAGA GTGATTTTCT 200  
ATTATAAACT TTCTTAGGAG CCAATACAGA GTAGAAAGAA ATATTTTCAG 250  
20 AAAG 254

## (2) INFORMATION FOR SEQ ID :862:

## 25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 300 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :862:

35 GTTCCTCCTT TGTAATTAT GAAATATTTA TAGTTTAGAC TGAGTAATAT 50  
GACATGAAAC AACAAACCTG CACATTTCTA ATTTATAACA AATCCGTTTC 100  
CTTAATGGGT GGAAGGAAAT CTGAGGACAA TTCTAAGGAG TCTTGCTGTC 150  
40 TTTCAGTGCG ATCTTCTAGT CATACTGAAG ACAATACCTC TCCAGATTGA 200

435

TCTTTCCCCT TCTTATACTC TTCCCGATCA ACGTCAATCA CACGCACCAC 250  
TCCAGGTTTT AGACTTAGGT CATCCGTCTC TACCTGACTT CTGTTGCCCT 300  
5 TCACCTACAC GTGGCTCGCT TTAGTTTGCT GAGCAGC 337

(2) INFORMATION FOR SEQ ID :863:

(i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 169 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :863:

TGGTGGGTTC GAGCCCAACT TCAGCGCTCT TCGAGAAGTG CGAGGCGAAC 50  
20 GGTGCGGGGG CGCCTCTCCT CTCCACCTTC CTGCGGGAGG CCCTGCAAGC 100  
TCTCAGCGAC GACGCCACCA TCTTCTGACC AACTTCAGGC TACTACCCCA 150  
25 ACTTACAATG CCACCGCGA 169

(2) INFORMATION FOR SEQ ID :864:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 286 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :864:

ATTAAGGTAA AGGAAGACTT TCCATTGTGA AGTAGAAAGA GTGTCCTGCT 50  
40 ATTACTACCA TTCACATCTA GTTTGTGTGA ACTAGGGTTT TCTATCTTAA 100

436

	CCCTGTAA AACAAGGAA AGAAATGGGC TGAATGGCGC ACCAGCTATG	150
	CGGATAGCAT TATCTTCCTG TGTTCAGAC TGAATGAAT TTATGAACAA	200
5	GGCAAGCACA CCATTATAGT AAATAAAATC TTACCTAGTT TTCGTTTTTG	250
	CATTTCTTAC TTCGCAGTAT TTCTCCCGCC AAGAGC	286

## (2) INFORMATION FOR SEQ ID :865:

10

## (i) SEQUENCE CHARACTERISTICS:

- |    |                            |
|----|----------------------------|
|    | (A) LENGTH: 272 base pairs |
|    | (B) TYPE: nucleic acid     |
|    | (C) STRANDEDNESS: double   |
| 15 | (D) TOPOLOGY: linear       |

## (xi) SEQUENCE DESCRIPTION: SEQ ID :865:

20

	ATATAGTCCG CTAGGGATAG TGAAAAATTT GGGGCTTGGT TTAGATTGGA	50
	GAGGTATATG GTGGGGTGTC TTATAAGGCT TAACTTTGGG AGGGCCCAGG	100
25	GCCTTGATTT CTGTCCCCCT TGCCTTGCCT GGCCTTTGAA TTGAAAGCTT	150
	TGAATTAGGC CTTCATAGAT TTAGTGTGC ATACAAATAA CACGATCTTT	200
	TTATAAGGCA GATTATGATT CTGAAGGTTT AGTGTGGGAC CCAAGCTTTC	250
30	GCATTTCTGA TCTATAAGGT GA	272

## (2) INFORMATION FOR SEQ ID :866:

35

## (i) SEQUENCE CHARACTERISTICS:

- |    |                            |
|----|----------------------------|
|    | (A) LENGTH: 296 base pairs |
|    | (B) TYPE: nucleic acid     |
|    | (C) STRANDEDNESS: double   |
| 40 | (D) TOPOLOGY: linear       |

437

(xi) SEQUENCE DESCRIPTION: SEQ ID :866:

ATGCAGGAGA AGAAGGATGC CAACTAAGT CAAAAAACG GAACGCAAAT 50  
5 AAAAGGAATG AGCACGGTTA CAAAGTCACA GGATGAGTCC CTGGGATCTG 100  
GGGCGGGAGA AGGGGTGAAT CAAGAATGAC TTGAGCTTGT TACTCCCTAG 150  
CAGGCTGAGG GCGTGACACA GCAGCTCGAT GACAAAGAGG TCTATTATAG 200  
10 TTTCTAACAC TACAACGCTA ACTTTTGGA ACGTATCTACT TCTAGCATGT 250  
AGACAGATCT CTAATCGCCT GCCAGACGGT AAGCCGCAGG AATGCC 296

15 (2) INFORMATION FOR SEQ ID :867:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 241 base pairs  
(B) TYPE: nucleic acid  
20 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :867:

TATTTTATCT CAACATAATA AAAACGACTA TAAATCTTCC TAAGAGAATG 50  
CTCTACTCCC AAGACTAATT TAAACTCGGG GATCGTCAGA GGGAGTGCCA 100  
30 CTGTGACTTC TACGATGAAA GAACAAGGA GAGAAGATCT TATCGACAAT 150  
CATACAAAGC CATATATACG CTATTCCTCA ACTCACAGAG TTAATTAAAT 200  
35 GTCACCAGGA TGGAAGAAAC CTTATAAGCC CCTATCTATC A 241

(2) INFORMATION FOR SEQ ID :868:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 130 base pairs  
40 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double

438

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :868:

GGACGACTGC AAGCTGGAAC TACACACGCG CACTCGCTCA CACTACACAC 50  
ACGCCACTCT CACACACTCT CACACACGCA CCCTCTCGCG CATGCTCTCT 100  
CAAAGCCCCAA TATAACCAAG GGAAGGAAT 130

(2) INFORMATION FOR SEQ ID :869:

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 310 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :869:

TTCAAATATT TATGTATGTT TGAACATTTT CATAATAAAA TGTGAAAAA 50  
CTAATGAGAA TGGCATAAAC AACATTTAAG CAATATATTT TGAAATTTAA 100  
TTCAAATGGT CAAATTCCTG GAAAACACAA ACTCCCTTCA CTAACAGAAT 150  
TGATAGAAAA TCTGAGTAGT TCACCATTGT TAAAGAAATG GAATGTGCCA 200  
TTTAAAACCC TCCAATTGAA AATACTACAT ATAGTTACAA TAGGGAATTT 250  
TCCAAGCAC TTAAACAATA AACAATGCCC TCTTTATACA AACCTTTCCC 300  
AGTAATAGAA 310

(2) INFORMATION FOR SEQ ID :870:

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 192 base pairs

439

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :870:

AAAGAGGCAA GTTCCTGGTG CAAAGGTGGC TCTGCAGCAT AATTTAGGCA 50  
10 TTGGAGGAGC TGTGTGTTGT AACACTCTAC AAGATGGGTT TTCCGGAAGC 100  
CGCCAGTTCT TTTAGAACTC ATCAAATTGA AGCTGTTCCA ACCAGCTCTG 150  
15 CAAGTGATGG ATTTAAGGCA AATCTTGTTT TTAAGGAGAT TG 192

(2) INFORMATION FOR SEQ ID :871:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 250 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :871:

ACCATAGATG TGTTCCAGAG GCAAAAGAGA CACATTATCC TAGATGGCAG 50  
30 AACATGCTTT CAAAACATAT AAAACGTCAA AGTTCCAGAT CTTTCTACAT 100  
TTTAAATCCT GTCTGAGGAT GGCAGCTGAC TTTATGTAGC TGATAGACGA 150  
35 CTAGAGTTTC ATCCAAATAC CTGACCACGA CTTTCATGGAG ATTTGAATAA 200  
TCTATCCGAT GAGATTTATA TNTAAACAAC TCAACTCCTG TCGAAACAAA 250

(2) INFORMATION FOR SEQ ID :872:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 313 base pairs

440

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :872:

10	TCAGCTACGA ATTGCTTCCT TCTCACAGAA CTGTGACATT TATCCAGGGA	50
	AGGATTTTGT ACAACCACCT ACCAAGATTT GCGTGGGCTG CCCCAGAGAT	100
	ATACCCACCA ACAGCCCAGA GCTGGAGGAG ACACTGACTC ACACCATCAC	150
15	AAAGCTTAAT GCAGAGAATA ACGCAACTTT CTATTTCAAG ATTGACAATG	200
	TGAAAAAAGC AAGAGTACAG GTGGTGGCTG GCAAGAAATA TTTTATTGAC	250
	TTCGTGGCCA GGGAAACACA TGTTCCAAGG AAAGTAATGA AGAGTTGACC	300
20	GAAAGCTGTG AGA	313

## (2) INFORMATION FOR SEQ ID :873:

25	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 270 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
30	(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :873:

35	TAGATGCTGA TGGCAATGAC ACAATTGACT TCCCTGAATT CCTGACAATG	50
	ATGGTAAGAA AAATGAAAGA CACAGACAAT GAAGAAGAAA TTAGAGAAGC	100
	ATTCCGTGCG TTCGATAAGG ATGACAATGA CTATATTAAC GCTGCAGAAC	150
40	TTAACCATAC AATGACAAAC CCCGAAGAGA AGTTAATAAA TGAAGAAGTT	200

441

GATGAAATGA TCAAAAACGT AGATNATTGA TGACGATGGT AAGGTAACT 250  
ATCCAGCGTT AGCACAAATG 270

5 (2) INFORMATION FOR SEQ ID :874:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 229 base pairs  
(B) TYPE: nucleic acid  
10 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :874:

TTGGGCCATG TCCCCATTTT ATCTCCAAAG CCAGCCATGG TGTATTTCTC 50  
TCTGCTTTTC TTCCATATTT CCAACCCAGA AATGACTCCT GTTCCCATAT 100  
20 GTGATTATTA TATTGCGCTA ACCCAAGTGA TTAAGGATAA TCTCACTACT 150  
TAATGACAGC TGATTATTTTC CATCTGCAAA CTTACTCAAG AATGCAATCC 200  
25 AGACTAACAC GACAATAGGA CATCAAGCT 229

(2) INFORMATION FOR SEQ ID :875:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 294 base pairs  
30 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :875:

TTTGAAC TTT CAGCCGAATA CATCTTTTTC CAAAGGAGTG AATTCAGGCC 50  
40 CTTGTATCAC TGGCAGCAGG ACGTGACCAT GGAGAAGCTG TTGTGTTTCT 100

442

TGGTCTTGAC CAGCCTCTCT CATGCTTTTG GCCAGACAGA CATGTCGAGG 150  
AAGGCTTTTG TGTTCCTCAA AGAGTCGGAT ACTTCCTATG TATCCCTCAA 200  
5 AGCACCGTTA ACGAAGCCTC TCAAAGCCTT CACTGTGTGC CTCCACTTCT 250  
ACACGGAACT GTCCTCGACC CGTGGGTAAC AGTATTTTCT GCGT 294

## (2) INFORMATION FOR SEQ ID :876:

10

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 173 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
15 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :876:

20

ATTTTTGGTA ACATACATCA AGTGGCACTA ATTACACAGT AACTATAAGG 50  
TAACTAACAT GAAACCACAG AACTGTA ACT CTGCCACAGC TGCATGAACT 100  
25 CGGGTTGTCC TGACCGAGCC CATCCCCAAA AAACCGCCCA CCCCAGAGCT 150  
ACGCCAACAA AAACCGTTAT TAA 173

## (2) INFORMATION FOR SEQ ID :877:

30

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 143 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
35 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :877:

40

TAATCAAAG AGCTCTAAAT CTGTAATTTC TTTCTCCTTT AAAAAAATGT 50

443

CTACTTTGTT TTGGTCCTAG GCATTAGGTA ATATAACTGA TAATATACTG 100  
AAACATATAA CGGAAGATGC AGATGATAAA ACTAATTTCG AAC 143

5 (2) INFORMATION FOR SEQ ID :878:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 base pairs  
(B) TYPE: nucleic acid  
10 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :878:

ACTGAATAAA CTGCTGATGT CCAGGTTTCAG TGGTTCCTGC TGTGGGACTT 50  
GCGTTTTTCAC TAAGTGTTGGC GTTAGATCCA TTAGTCCCCG AAGAGCCTCC 100  
20 AGTGCTTCCT AATGCCCCCA AGCCAGGAGT AAACCCTGGA ATGAGGCCCA 150  
GGGCTTCTAT TGCTAATGCC TGTAACCTT GCTGAATCTA TAACAGAGTC 200  
25 TATACCGCTC TCG 213

(2) INFORMATION FOR SEQ ID :879:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 227 base pairs  
30 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :879:

AAAGAAGGAA AAGAAAGAAA TAACACTTAA CAGTCCATAA CAAAGTGTTA 50  
40 ACGAGATAGA CACATGCTTA TTCAAACCAC AGATATGATC CAGTTAATTC 100

444

CCTTCTTAGA ATGTGCCCCAT AGTGCCTTAT TGCCTCATAA TAATGATAAT 150  
AATAAGAGCA ACAATAATAA CGGCACAAAC TCCAGTCGAT ACTGACAAAC 200  
5 TACCAGAGTA ACCGTCATCC CCTTGAG 227

(2) INFORMATION FOR SEQ ID :880:

(i) SEQUENCE CHARACTERISTICS:  
10 (A) LENGTH: 221 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear  
15

(xi) SEQUENCE DESCRIPTION: SEQ ID :880:

ATAGACAAAG TCCTTCCCAC TAGAACTTAC ATTCCAGTGG GAAGAATTAG 50  
20 AAGCCTCAGG AATTCCATTG CTTACTTTTA GTTGTTACTT CAAAAGTACT 100  
TACATTTAAT CTGATTATTA ATTATTCGTC ATGAGCTTCA TTTTATTACA 150  
25 TCCAGGGCAC AGTATGTGAA TTGTGTTTCG TTCCTTTAGG AAAAGGAAAA 200  
ATAATCACTC TTTACAAGGT A 221

(2) INFORMATION FOR SEQ ID :881:

30 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 310 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :881:

40 AATTGTGGTA TATTTCAATT AAAATCGATC AAAGACAGCA ACATACATTA 50

445

ATCAGAGGAA AGCATCAATT AAATGCAGAA ACAAGATTTA AACAAAGATT 100  
CATATTAAAA CAATGATAAG TAATACTTAG AAAGTGCATC CTAGAGACAC 150  
5 ATCATTCGCA TTTTGTAGAA AACAGAAACA TATTAGTGTG AAAAGATGTT 200  
AAAAAATGAA TATTAAACCG TCGAGCACAA CACACTACGC CGATAACAAT 250  
ACACCACAAG CGCCGTAATC CTGCCGACAC TGACACACTA CAGGCGTCGT 300  
10 GGCGATCCGA 310

(2) INFORMATION FOR SEQ ID :882:

15 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 177 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :882:

25 GTTCACATCA GTGTGTAGGA TATGCTATCA CGTATGTGCA TGAGAAGAAT 50  
GGAGAAAATG GATCTATGCG GATGTCTGTA CACACACACA CACACACATA 100  
CACAACAAGC TTGCACATGT ATAGAGGATC CGAAATTCCA CCAATACTGA 150  
30 CGAACTACAA ACGTAACAGC AGCAGGC 177

(2) INFORMATION FOR SEQ ID :883:

35 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 152 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

446

(xi) SEQUENCE DESCRIPTION: SEQ ID :883:

CAATTCTATT TTCAGAGTTG ACTGTACTCT TTTCTCTGA AGATACACGT 50  
5 ATAAACGCGA CCAACGAGGT CTCTCGTCCT AATAACAGGT TCAGGCATGA 100  
ATCACCGTCT AACAGCTATT TAAACACCGC CTCTTCATAG AAGTAACGCC 150  
GA 152

10

(2) INFORMATION FOR SEQ ID :884:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 177 base pairs  
15 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :884:

CCATAATATA AGTATTTATC ATGTATTCTG TGTCTGGAAT ACAATTCAAT 50  
25 GACCTATTTT AGAAAAATCT TTTCAAGTAC TGGCTGAAAG AGTGAGGGAT 100  
ACATTAGGAG ACTGCAAATA AACTGGCAAT CACAAGAACT TTTTCGGATA 150  
AAATGAAATT GTGCCGAAAT GTATACA 177

30

(2) INFORMATION FOR SEQ ID :885:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 241 base pairs  
35 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :885:

447

5 CACAGCTGGA AGAGCGGAGA AATAGAATTG TCTTCAAACA ATATAAAAAT 50  
TCATAAAGAA TAGAAAGACT ACTATGTGTG GGTCCGGGAAA TTAAGTAGAA 100  
TTTTTTTATA TCCACACTCT AGTATGAAAT GAGTACTTAT AGAGTAGAGT 150  
GTAACATATT TAGACATAGT ATATATATAT ACAAGTGTA CAAATATATA 200  
TATTAAATAT ATATATGTTT TATAGAAACA CAGAGCACAC A 241

10

(2) INFORMATION FOR SEQ ID :886:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 190 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :886:

GTAGCAACCG GCGCTCAATA AAATTCAACC AGCAAACCTCG ACAAGTAACA 50  
25 ACCATAAAAC CAGCCACACT AAGTCCAGCC ACCACTACTC AATAAAAATA 100  
ACACGTATCT TCCACCGTAC AACCAATAGC AACTGCAGGC TACTGCAACG 150  
CCATCCATAT ACCAAAAATG CTACTTACAA CACCACAACA 190

30

(2) INFORMATION FOR SEQ ID :887:

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 168 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :887:

448

CACGCTTTCT CTCACACAGC ACTAGCGCTC TCTCACTATC ACTCTTCTCA 50  
CAGAGCTGCG CGCGAGTCTC ACTACTATCA AATATATCTG TCTCTTCTCA 100  
5 CTCTATAGCT CTCTCACAGA TATATATCTA CATATAGCGC TCTCATTATA 150  
CTATAATATT ATACTCTC 168

## (2) INFORMATION FOR SEQ ID :888:

10

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 15 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :888:

20

ACTGGGCGCG CTGGTGCTGA CATCTTCAAG AGCATCTGTC ACTGAATATT 50  
GCCGATCTCG CAACCGGTTT CAGTTAGACA GAACATTGTG ATATTCAAAC 100  
25 CACTTTCTCG TAATTTCCAA TGGAGTTGTA AAGTTTAATG AGACCTCGAT 150  
AATCATATTC TAGTCCACTG TAGC 174

## (2) INFORMATION FOR SEQ ID :889:

30

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 327 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 35 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :889:

40

ACACCACACT TAAGGAATGG GAGTTATATT TCACTTCCCT GAGGCCAGAA 50

449

TATATATATG TATGTATGTA TATGTGTGTG TGTGTCTATA TATATATATA 100  
TATAGACACA CACGCACATT ATACACACAT ATATATACAC ACACATATAT 150  
5 ATATGTGTGT GTACAATATA TAAAAAATTA TATGGGAGAA AAGAAAGGCA 200  
AATCTCCCAT GGCAGAGAGG TATCCCAAAA AATTTTTTTG TGTGTAACAA 250  
AATATGTTGT GTGTATATAT ATATGCACAC ATATTATGT GTATATATGT 300  
10 ATATATATAT CTGTATATAC AGGTATA 327

(2) INFORMATION FOR SEQ ID :890:

15 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 181 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :890:

25 TTTTTTTCTT GTCTCTCCCG CAGCGCGCGC CTCTCGCGGC GCTATCTCTC 50  
GCTCTCTCTC GCTCTCTCGA GCTCTCGAGA TATAGCCGAG ACACGAGAGC 100  
TCGCTCTCTC CCGCGCGAAG ATCTCACCCC CGCGCGCTCG CGCGATATAT 150  
30 ATCTCCTCGC GCGCGCGCCG AGCGCGCCCC T 181

(2) INFORMATION FOR SEQ ID :891:

35 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 207 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

450

## (xi) SEQUENCE DESCRIPTION: SEQ ID :891:

	CTCTTTAATA GCAAGCGAAT GGTAATTACA TGGTCGGATG AGGTCCTCAC	50
5	TCTCAGGGGA GGGAGGAGGG AGCAGAGGTG GACAGGGTGC AGTATAGGAT	100
	TTACACTGTT TGAAGCATCT AACGAAGGGC AACAGTTTTT GGCAACCCAA	150
	TTCACAGTTT TGTAATTTAC AAGAGATTTC TTTGAAAGGA AATAGGAAGG	200
10	CAAAGAA	207

## (2) INFORMATION FOR SEQ ID :892:

15	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 198 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear
20	

## (xi) SEQUENCE DESCRIPTION: SEQ ID :892:

25	CTATCACTTC AGGGAAACAA ACAACTAACA GCCATCAATT CAGAGGGAAG	50
	TGATTTTACA GTAGAGTGAA CGAACTTGG GAAGGAAAAC ATCCAAGAGG	100
	CGTCTGTTTG ACGTGGGTAA CGTGGGGAAC GCATACTGTC TGGCAAGAAT	150
30	TCTACTAGGA CCACGGGAAA CAAAGCAGAT TAAACACTC TCTACTCT	198

## (2) INFORMATION FOR SEQ ID :893:

35	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 96 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear
40	

451

(xi) SEQUENCE DESCRIPTION: SEQ ID :893:

CTTTAGAGAA TGCCTTGTGG AAAAAAAAAA AAATGGGCCC CAATACTTTT 50  
5 TACTGCCCTT TATCAAAATT GTTGTGCATG GACCGGGCCA AATAAG 96

(2) INFORMATION FOR SEQ ID :894:

(i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 325 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :894:

AATTGTATAC CAACATATAA ATTAAAAGTG TTATGCAATG AGAAACAATA 50  
20 ATGGAACAG CATAATACTA CATACTATCG CGCGGGGTTG TCGGCGTGGT 100  
GGGCGTGCGT GTAGAGAGAG AGCAAGGGCG TGTGCGTGAG TGGGCGTAAA 150  
25 GAGTGAGCGT GGGAGGGTGT GGTCGGTGGA GGTGTGTGGA GAGGTGAGTG 200  
TGCGAGAGGG GCGAGTGTAT GTGTGATAAG TATAGCGCGC AAGAGGCGAG 250  
GACAAAATAT ATATATATAT AGATATAATA GATATGAGAG AACACTAAAC 300  
30 AATAACCACT ACTCACATAG AATAT 325

(2) INFORMATION FOR SEQ ID :895:

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 266 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

452

## (xi) SEQUENCE DESCRIPTION: SEQ ID :895:

ATAGTTGTAC ATTTTATGG GGTGCATGTG ATATTTTGAT ATGTGCATAC 50  
5 AATGTGTAGC AATCAAATCA GGGTAATTGG GATATTCATC ACCTCAAACA 100  
TTTATCATTT ATTTGTGTTG GAAACATTCA AACCTTTTCT TCTAGCTATT 150  
TATCCATTGT TGGATACTTA TATCAATTCT ATATCTTAGC TGTGTGAAT 200  
10 AGAGCTGCAA TAAATGTAGG AGTGCAGATA TCTCTTGAT ATACTGATTT 250  
TCTTTCTTTT GTTATA 266

## 15 (2) INFORMATION FOR SEQ ID :896:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 197 base pairs  
(B) TYPE: nucleic acid  
20 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## 25 (xi) SEQUENCE DESCRIPTION: SEQ ID :896:

AAGAAGAGTC TTCTGCACAA ACAAACCAT AGTGTTGACA AATAGTCATG 50  
GCCAATGGCA ATCTGATGGT CCAGCGGCCC TCGGATGACT CCTCTGCAAG 100  
30 GAGCATCTTC AGGGTTCTAG GGAAGTCACA GGGGCAACAT ATTGGAAACT 150  
AGCAGGCCCA GAAGACCGCC CCGCCCCCA TGCCCTGGCG CAGGGCC 197

## 35 (2) INFORMATION FOR SEQ ID :897:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 192 base pairs  
(B) TYPE: nucleic acid  
40 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

453

## (xi) SEQUENCE DESCRIPTION: SEQ ID :897:

5 GATGGCTGGA GTAGATTAGG GCGTAGGTAG AAGTAGAGGT TAAGGAGGGT 50  
GATGGTGGAC TATGATGGTG GGGATGATGA GCGCTATTGT TTTTGTGAA 100  
TATTTTCTT CCGACTAACT CGCGCCCCAC TCTCTGCGA GCACAAACAC 150  
10 ACGCGCGCGT GTAAGCGGCG CGAGACACGC GCCCCCTCCC CT 192

## (2) INFORMATION FOR SEQ ID :898:

## (i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 224 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID :898:

25 TGGATGTTTT CATTGCAAA TCATGAGAAA CTTAAGTGGG TTTTATGCAC 50  
TTGATAGAGT TGGCAAATT GAACTATGAA GTTAACTATT TAACTCAAGG 100  
AATGGGCGGC AAACCCATCC CCTCGATTGA TAAAGAAGGG GAACATTTTT 150  
30 ACATTAGAAC TGACACTGAA AACATAGCTC TTTTTCAGTC CACCCTGGTT 200  
GCTCTAGTAG CCCACAGCCC AATC 224

## (2) INFORMATION FOR SEQ ID :899:

35

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 362 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
40 (D) TOPOLOGY: linear

454

## (xi) SEQUENCE DESCRIPTION: SEQ ID :899:

	GAGGTGATTT CTCAGAGTTT AGAGAATAGG ATGGGGAAAA TTATATTTAG	50
5	TGAGTTATAA CCAGAATTAC ATAAGACAGA TATGGAAATT TTATAAACAA	100
	AATGCAAAAT ATTCTAATGT TTCAATGTTT TACATGAACA TATAGGGAAG	150
10	CATAGACAAT AGCCAAAAAT ATGTTCTGCA TTCATATACT AGTTCAAGTC	200
	CGAGTCTGGC TACTTTCTAG GTACTGTGCT TTTTGTCAA TTATAAAGAT	250
	ATATTCCTT TGTTTTTTGA AAACGAGTGA GATGCTTAA TAGAGTACAA	300
15	TTATCTCATT CAAAATGTAT GTTGTTCCT CTCGAGAATT GTGAAGGTTT	350
	TGAGATTTGA TT	362

## (2) INFORMATION FOR SEQ ID :900:

20

## (i) SEQUENCE CHARACTERISTICS:

- |    |                            |
|----|----------------------------|
|    | (A) LENGTH: 310 base pairs |
|    | (B) TYPE: nucleic acid     |
|    | (C) STRANDEDNESS: double   |
| 25 | (D) TOPOLOGY: linear       |

## (xi) SEQUENCE DESCRIPTION: SEQ ID :900:

30

	GTATGTAGCC CAGTGGGTGT CTTCCACAG GGTAGGTACT CAGTTTGCTC	50
	TGGAGGGTGA CTCATACCTA AACAAAGTGA CATCTCCTTT CTCAGTAAAG	100
35	CCAAAGCAGG TTTCTACATT TGGAACAAAA GAGATCCTGA CCAGAGAGCT	150
	ATCACTGGTG GTCCACTTGG GCCCTCCTTG ATGGGTGTGT TCACTTAGAA	200
	AACCAAATTA CAGATCTGAA GGCTGCTGGG TAGGGACAGG ATTAGAACAA	250
40	AGGGAATGAG ATTGAATGTT ATTTAAGGGA TATTTCTGTC AAGTTTTGGT	300

455

TTCTCGATGA

310

## (2) INFORMATION FOR SEQ ID :901:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 185 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :901:

15 TTCCCCCATG AGACCGTTAG TCTCTCTTTG CCTGGCTGAC TACCTGCATA 50  
CAGTAGGCAC TCACTGCTGG AGTGAGGCAC TGACTCCTCC AAAGATTGCA 100  
GGGGGCGGAG GAGGGAACCA CGAAGGCCTG GGAGGGGGCA TCTTTGGCCC 150  
20 CCACTAACCA TCTCCCTATT TCTGCATCCT GGTGA 185

## (2) INFORMATION FOR SEQ ID :902:

- 25 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 381 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :902:

35 ACAAGCTGCA AGATCCTTCA CTTGAGGCTT TCAGCCTTAT TCTCCTCCTG 50  
TCAAACAACCT AAATACTCC GATGTTTGAT GAAAATTAAA CTGCTACTCA 100  
GGATACTGCA ATTACAAGGA GAGGGAATGA TCAGCCCAGG GAGGCTATTA 150  
40 CGTGTGACCT TTGAGATGGA CCTGATCGCC CCTTTTACTT TTTAGACTAC 200

456

AAGTGCAGGG AGGTGGAGCT TATTTGCATT TGAAGTCCCTG TAAAGAGTAA 250  
GAATATGGAA AGGATGAAGC CTCATTCATT CGGGCATATT AAAAAGAAAT 300  
5 TGCCTTCAGA AACACTTTGC CTTTAAATAT GTGTAGCTAC AGTAAGTACC 350  
AATGGGGCTAA CTAATTGAAG CTAACATTTT A 381

## (2) INFORMATION FOR SEQ ID :903:

10

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 240 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
15 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :903:

20

CATCAAGGGT TTTTCCTGCT GCAATTCTTG TCAAAAAGTAC ACATATGTAT 50  
ATCGTTCTCA ACTGGCAAGC TGTTAGACTG GATAGTCCAT GAATAATAGC 100  
25 CTCTGCGCTG TTGCGGGTCC TCGGGAAGTC CTCGGAGCGG CCGTCGCGGA 150  
AAGCTCGGCA AAGAGAGAGG CAGAGGAAAT CGAGCATCCA GCCGGCAGCC 200  
ACTTTTTTTT TATCGGCACC AGGCCGCGTC CTCCTCCTCC 240

30

## (2) INFORMATION FOR SEQ ID :904:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 280 base pairs  
35 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

## (xi) SEQUENCE DESCRIPTION: SEQ ID :904:

457

CCCTGGGCAG GCTGCTGGTG GTCTACCCTC GGACCCAGAG GTTCTTTGAG 50  
TCCTTTTGGG GATCTGTCCA CTCCTGATGC TGTTATGGGC AACCTAAGG 100  
5 TGAAGGCCTC ATGGCAAGAA AGTGCTCGGT GGCCTTTAGT GATGGCCTGG 150  
CTCACCTGGA CAACCTCGAA GGGCACCTTT GCCACACTGA GTGAGCTGCA 200  
CTGTGACAAG CTGCACGTGG ATCCTGAGAA CTTCAGGCTC CTGGGCAACG 250  
10 TGCTGGTCTG TGTGCTGGCC CATCACTTTG 280

(2) INFORMATION FOR SEQ ID :905:

15 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 225 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear  
20

(xi) SEQUENCE DESCRIPTION: SEQ ID :905:

25 GTTCTAGTGG TAACTGCTGC TTCTGGAAAA TATTTAGAGA AACCAACGGT 50  
AAAAAAAAAA ATAATAATTA ATACCGTTGG TTTCTACATA CACTCTCAAT 100  
ATTGTCACGA GTAAAGCGTA GCAAGTTTAA CACAACCTAT GTAAACTTGG 150  
30 AAAATTTTCC GAAATTTTAT TGACTTTTCT CGGTCTCTCC TATCTTTATA 200  
TACACATCTC TCATGCACAC ACGCG 225

35 (2) INFORMATION FOR SEQ ID :906:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 161 base pairs  
(B) TYPE: nucleic acid  
40 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

458

(xi) SEQUENCE DESCRIPTION: SEQ ID :906:

5	GGTGCTGACA TCTTCAAGAG CATCTGTCAC TGAATATTGC CGATCTCGCA	50
	ACCGGTTCCA GTTAGACAGA ACATTGTGAT ATTCAAACAC TTTCTCGTAA	100
	TTTCCAATGG AGTTGTAAAG TTTAATGAGA CCTCGATAAT CATATTCTAG	150
10	TCCACTGTAG C	161

(2) INFORMATION FOR SEQ ID :907:

(i) SEQUENCE CHARACTERISTICS:

15	(A) LENGTH: 204 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :907:

25	AGAGATATAT GCAATCTGGT AGTCCATTAA ATGAGAGTTA CACTTAAAAT	50
	ATTTTAGTTC TTTTAAAGAA AAAGTCTCCA TGTGCTATTT GGGAAAACCT	100
	TCATTGCCTA AAGACCCACT TGCATAATTA AGGCAGATGA TGATGATCTT	150
30	TATATATGCG CACACACACA CACACACGAC ACGACGACAC ACACACACAC	200
	TCTA	204

(2) INFORMATION FOR SEQ ID :908:

35

(i) SEQUENCE CHARACTERISTICS:

40	(A) LENGTH: 316 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

459

## (xi) SEQUENCE DESCRIPTION: SEQ ID :908:

	AGTTTCTGCA TTTGGTCTGT GTGACTCTAT GGAGCCCAGG ACTTACAGAA	50
5	AAAGGTGTAA CTGGCTCTTA GGACTTTAAG CCACATTATG GTAGTAGACC	100
	TGCCGTTTTA TTTGACATGG TGAAATAAAC TACCACTCCT TTGTGGTACC	150
	ATATGGGCAG GACAGAGCTC TTCAACCCTG GCTAACAAGC CTGAAGAAGA	200
10	CCCTGTGAGG CCGCAGCAGC CATGGGAACT TCCCAAAGGA CAGAAATCCA	250
	CATTGGAACG TAGCATCCAG ATAGGTGACA GAAATTCCTT CCACCATATC	300
15	CAAATGTGTG TGTTTT	316

## (2) INFORMATION FOR SEQ ID :909:

## (i) SEQUENCE CHARACTERISTICS:

20	(A) LENGTH: 307 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID :909:

	CTAGTAACAT AGAAAATAAA CTTCACTGGG AATCTCTGCT TCCCGCGTGA	50
30	GGTGTTTAAT TCTTGGCATT TTTGTATTTT AAAGATGTAG CAACTTGTTT	100
	CAAGTTAGAG GAGATGGCAG GGTCAAATT TTAGAACTG GATCCCACCA	150
35	CCACTGTGTT ACTTCCTAAA CCTGCATACA AATGTTCTGC CAACATGTAA	200
	TGTGCCAATA GAATTATACG GTGTGAACTG CATATCTCAG TATCTCCACG	250
	GGAAAAAACT GTGGTTGGGG CATGGAGGGG GGAAAGGGAA ACTTTTTTAA	300
40	GCTATTT	307

460

## (2) INFORMATION FOR SEQ ID :910:

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 172 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :910:

TTTTTTTTTT TTTCCAGGCA CCTAACGATT TGTTTGTCTC AATCAAACGC 50  
15 AGACAGGCGT CTCCGAAGTA CCACCACTGG GATATCCTCG GACCAGCGCT 100  
TAAACCGAAT CCCACAATC TCAAAC TCAA CCAGGCCAAA GGGAACACAG 150  
TGACACAACA ACAGGGTTCC AA 172

20

## (2) INFORMATION FOR SEQ ID :911:

## (i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 255 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :911:

GCATAGAGAG ATATATACAC AGAGAGGACA TACATATATA TATATAGAGA 50  
35 CACAGAGACA GACATATAGA GATATATATA TACACAGCAT AGAGATACAG 100  
AGAGATAGAG AGAGATACAC ATACACACAT TCATCAACGA GAGAGAAGAG 150  
AGGAAAGAGA GAGAGAGCGA GCACAGACAG AGATAGAGCA CACAGAGAGA 200  
40 TCGCGCAGAT CTATACAGAG GGATATTCAC CACATTGTAT ATGGAAAGCG 250

461

CATCT

255

## (2) INFORMATION FOR SEQ ID :912:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 196 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :912:

15 CAAGCGAATG GTAATTACAT GGTCCGATGA GGTCTCACT CTCAGGGGAG 50  
GGAGGAGGGA GCAGAGGTGG ACAGGGCGCA GTATAGGATT TACACTGTTT 100  
GAAGCATCTA ACGAAGGGCA ACAGTTTTTG GCAACCCAAT TCACAGTTTT 150  
20 GCAATTTACA AGAGATTCTT TTGAAAGAAA ATAGGAAGGC AAAGAA 196

## (2) INFORMATION FOR SEQ ID :913:

- 25 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 203 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :913:

35 ACTATCACTT AAGGGAAACA AACAACTAAC AGCCATCAAT CCAGAGGAAA 50  
GCGATTTTAC AGTAGAGTGA ACGAACTNG AGAAGGAAAA CATCCAAGAG 100  
GCATCTGTTT GACGCGAGCA ACGCAAGGAA CACATACCGT CTGGCAAGAA 150  
40 TCCCACTAGG GCCACGAGAA ACAAAGCAAA TAAAACATT ATCCACTACA 200

462

CGA

203

## (2) INFORMATION FOR SEQ ID :914:

5

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 262 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :914:

15

CTGCCGAGCC ACCATGCTTG CCTGAAGCTT CGGCCGCGCC ACCCGGGCAA

50

GGGTCCTCTT TTCCTGGCAG CTGCTGTGGG TGGGGCCCAG ACACCAGCCT

100

AGCCTGGCTC TGCCCCGCAG AACGGTCTGT GTGCTGTTTG AAAATAAATC

150

20

TTAGTGTTCA AAACAAAATG AAACAAAAAA AAAATGATAA AAAAATCGGA

200

TTTCCGGTTA ACACTGTGAC TTCAATTGAA ACACCTTTTT GTAGTATCTG

250

25

GAGGTGGACA TT

262

## (2) INFORMATION FOR SEQ ID :915:

30

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 191 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

35

## (xi) SEQUENCE DESCRIPTION: SEQ ID :915:

TGGGTTCTAA TGATGTGCTT GAAGAGGAAG ATTTTGATCG CACCACTGAT

50

40

ACACGGAGTC TGTATTTTGC ATCCTAGAAT GATTAACCAG AAACAAAGAA

100

463

AGGAAAAAGG TAAATCAAT AATAAGATCA GCAGCTCTGG GACACAGAAT 150

AAAGAATGAA ATAATTTGAA AAAAAAGGCA GGGCAGGCAA A 191

5 (2) INFORMATION FOR SEQ ID :916:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 252 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :916:

AGACTTGGGG GTTCCTGGTG TGTGAGGGGT CCTGGGATAG CTAGGGGTTT 50

TCCAGGAGTT GTCCTTTGTT GTTTGTCGTG AAGAATTATA CTTTGTGTGT 100

20 GTGTGGGTTG TCCCATGTGT ATGCGTGTAG TGTGACAGTA TATGACCCCC 150

AGTGTGTGCA TATGTTTGTG TGGTTGTCTC TGAGTGATAT CCACCTCTCT 200

25 CTCCCCCTCT GTCTCTCTGC AGAGATATGT GTGGCGTCAC TGTACTCTTG 250

TG 252

(2) INFORMATION FOR SEQ ID :917:

30

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 247 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :917:

40

TAGACAGAGT GACAGTGAGA GAAAAAGAGA GGAAGGAAAA GGGAAAAGGA 50

464

GTAGGGAAGG ATGAGGGAGA TAGGAAAGCA CCTAC GAG GCAGAGAGTT 100  
TCCTGAAGGT CATGCGATCC TTTACCCTCA GAAACTTTCA GGCTGAAATC 150  
5 ACCATCTCCG TTATCCCAAC AAACGCACTC TCCTACCTCT ACAAGCACTT 200  
CAAGTAAAGC AGAAATCACA CCAATACTGA CGNGCTTCAA GCGCAAC 247

## (2) INFORMATION FOR SEQ ID :918:

10

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 191 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 15 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :918:

20

ATTTGGATTC AATTGCCTGT TGCACCTTTTA CATTAAGTGT TGCTTAAATA 50  
AACAAAAATA GAGCATAAAT TCAATATTCT ACTGTCTAAA CATTTTAAAG 100  
25 CAATGGTTAT GCCATCATAA ACAAGTAAAA TGCACCTAAT TCGAGTCTTT 150  
TGACACCTCT TGTTTTAAGT TTCCTGTATG ATAAAGTTCT T 191

## (2) INFORMATION FOR SEQ ID :919:

30

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 205 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 35 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :919:

40

CAAGAGTGAG ACTCCATCTC AACCAAAAAA AAAAAGAAAG AAAAAAGAA 50

465

ACAACCTCCT CATTTTCAGA AGCGAACACA CCCCCGCCCC AAGATAGACG 100  
ACAGAGACCG GACTAAGATT TAACCCAGGA ACTTTTCGCT TGGGCACCTT 150  
5 CGAACAAACAC ACAACCCGCA AAACCATACA CGCTCCCTTG CCCGAGGCCC 200  
AACCC 205

(2) INFORMATION FOR SEQ ID :920:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 323 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :920:

20

GACAAAATTG GGA CTCTAAG TATTGCGCTT TTTTTCCTC TCCAACGACT 50  
CGTTCCCTTT CAACAAATAG CACTTCAGTC CACTGTGTAC AGAAGTAATA 100  
25 CATCTCCTAT CGTTAGTTGA ATAAATTCAC ACACGCGTT TAAGAGATGA 150  
AACCACGACT TCGTCAAGCC ACATTCGATT GCCATAAGAT TCCAAAGAAT 200  
TCTATCCTCT TAAAGCGAAC CACATGTAAC CCGAAGGTCC CCACCTATCA 250  
30 AGGTTAGAAC TGATATTCAA ATTATAGACT CATTCCACTA AGCAAGTAAG 300  
CTCTAAGCTA CAGGTTGATC ATA 323

35

(2) INFORMATION FOR SEQ ID :921:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 230 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
40 (D) TOPOLOGY: linear

466

## (xi) SEQUENCE DESCRIPTION: SEQ ID :921:

5 AACATTGACG ACGCTAAGGA TGCCATGATG CCATGAATGG GAAGTCTGCA 50  
GATGGACGGC AGATCCGAGT AGACCAGGCA GGCAAGTCGT CAGACAACCG 100  
ATCCCGTGGG TACCGTGGCG ACTCTGCTGG GGGTCGGGGC TTCTTCGTG 150  
10 GGGACCGAGG CCACGGCCGT GGACTCTCTA GAGGCGGCGG GGATCAAAAC 200  
TATAGAAACA ACAAGTTAGA GTACAGACGT 230

## (2) INFORMATION FOR SEQ ID :922:

15

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 239 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
20 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :922:

25

TATTTTTCCT GATGTTCTCC CTTCTCCAG TCCCCGACCT CCCACAGGCC 50  
CCAGTGTGTG TTGTTCCCGT TCCTCGTGTC CGTGAGTTCT CATTGTTTCT 100  
30 TGCCCATTTCT GAGGGAAAAC ATGCCAGTGC TTTGCGGTTT TTCCTCGCTC 150  
TCACCCACCT CTCAGCTTAT CGCGTCGCGC GCGCAGTATA TTCGTCTCTC 200  
TCTCCAGTCT CTCTCGCGAC ACACATCTCT CTTTTGTAA 239

35

## (2) INFORMATION FOR SEQ ID :923:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 178 base pairs  
40 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

467

## (xi) SEQUENCE DESCRIPTION: SEQ ID :923:

5 GTCAGTTCAG TTGTGAACAA AGCCCTTTGT GTACGTTTTT AAATTTTAGT 50  
TCACACGATA ACAATGCTTT GCAAGTAGGT GTAATTATTT TACTCCCATT 100  
TTATGGATGA GAAAACAACA GAGAGGTTGA TTGGCCCCAC CTTCAAATCC 150  
10 TGAAACCCGT CCACTCAATA AATTTTGT 178

## (2) INFORMATION FOR SEQ ID :924:

15 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 325 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear  
20

## (xi) SEQUENCE DESCRIPTION: SEQ ID :924:

25 CAGCTGGTCC CCCACTAAAA GAAGGGGCAG ACCACCACTA GCCAAAAGAG 50  
ATAGCAAGAC TAACATCTGG AAGAAGCGAG AGGAACGCCC ACTGATTCCC 100  
AAAAAAAAAAC TCCAATGGGG ATTGTGTGTC TGCTGTCTCG TGCTGTTTAT 150  
30 TCTTGCTTCT TGTGTAAAT TGCAGTACGA ACTTAAGAAA ATGAGACTGA 200  
GCAATCTCAT GGTTCCTGGA CATGTCTCAA GCAGAGTAAA TGGTAATTCA 250  
35 GTAATCAGAG AGAAAGATAC CAAGGAATGC TTTTCTGGC CTATTCATTT 300  
ATTTTGGGG GATGAATTTA CAGTA 325

## (2) INFORMATION FOR SEQ ID :925:

40

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 261 base pairs

468

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :925:

10	ATGGCTATGA CCTGGGACAT GGAAACAGTG ACCTCCGCGT TCTGGTCCCG	50
	AGATCCTCGC ATCAGCGTCA TCGTGTGCAC CGGCTTGGGG GGCTGGAGTT	100
	CCGGTTTTCT TTGTTTTTTC TCTTTATTCG TCCTTTCTCA AAGATGGGAT	150
15	ACTGATCAGA ATCGTTCTGT ATATGCTTGG GACTGGATGG AAAGACTTTG	200
	AAGCAGCTGT GGGGGGCGGG AGGACACCGA CAACCAAACA GACGTGTTGG	250
20	TTCCAGTCCT G	261

(2) INFORMATION FOR SEQ ID :926:

(i) SEQUENCE CHARACTERISTICS:

25	(A) LENGTH: 173 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :926:

	GTCAGCCTGG GCAATCACAA CGACAACAAA AGGTACAGTC TCAAGAGTCC	50
35	AACTGGGTTC AAATCCTGGC TCTGTACAT ACTAGCTGTG TGACCTTGGC	100
	CAAGTTTCTT AACCTCTCTG TGTGTATAGT CCTTATCTGA AAATGGGGAT	150
40	AACCAACCAA GAGAGCTGAG AGA	173

(2) INFORMATION FOR SEQ ID :927:

469

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 223 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :927:

10

AACACTCAGA CCGGACGGGA CGAGGGATTC CCCTGCCTTC GCTTCCCTCC 50  
CTCGCTTGCT TTGTAGTTTT CCCGCACCAG CCCGCTGCCC TCGCCCATCC 100  
TAGGGCCTCG AAGCCCGGGG AATCTGTCCC ATCCTGTAAC GGGCCGCCCC 150  
CTTNGATTTT TCTGCCCGTG CCACCGGAGG TTGCTGCGAC GCGCACCGAC 200  
TCAGATCATT ACTACTGAAC TCG 223

20

## (2) INFORMATION FOR SEQ ID :928:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 212 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :928:

GTTATAATTA TTTACATGCT GCAACACGTC ACAACATAAA TTTACCAAAT 50  
ATTCATGGT GGGATGCTGT AGGTTTCAGA TAATAGTTTT AAGATAAAAA 100  
CCACAGATTA AGTGAAGACA CCCACAACCTT TAATGACTCT ACGACTCTCG 150  
GTTGCTAAAT GCTAGAAGTC AAAAGGCAGT GTTTTTTCAG TCCTACCTGT 200  
CATAACTTGC AT 212

40

470

## (2) INFORMATION FOR SEQ ID :929:

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 233 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :929:

TTAACATAAT ATTTTGAATA TATAGGGCTC ATAAGATATA TTATTAAATT 50  
15 ATAAACAAAA TAATCAGGAA CTTAGTGTGG TGCCTAGTTT GATATATGAT 100  
TACTTTTTGA AATGCACTAA ATTCCACAAA TAATGAAAGT ATTCTTTGTG 150  
TATAATGTTA TGTTTGGTTA TTATGTATGG TCTTCGTATC CAAAGGTATG 200  
20 ACATAACTTG AGTTTGTTTG CTTGGTATTT ATT 233

## (2) INFORMATION FOR SEQ ID :930:

25

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 235 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :930:

35 AGTCTGTAAC GATACACCCA TAGATGTGAA TTATGTATAT TCGAGAAGGA 50  
GATCAGATGG CATCCAGAAG ATAGTTTAGA TTTCAGCACA TTCATGGTTC 100  
AGATGCAAAA TCAGATCATC AAATAGATCC AGCAATTCAC AATCATCATA 150  
40 GCCATATCGC GTCACGTCCG CCGCACAAAG ATCCGCACCA ATTATCTATC 200

471

TCCCACCCCC CCCAGGCATT CAGCACCCGC AAAAG

235

(2) INFORMATION FOR SEQ ID :931:

5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 221 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :931:

15

CTATCTAGAA TTACTTATTT CACTTGAAAT GTATGGTTTC AGGAAAATTT

50

TCAATTTAAC TTGAAGGGAT TATCTCTTAT TTTGCTTGGA ATAATGGCAT

100

CTCAGAAACA TGGGTTTACC TGTGATTTTT TTGTTTGGGT GAATGCTTAA

150

20

AAACAAAAAA AAAATTTACA TATGCATTTT ATGGATACAC ACACACACAC

200

ACACACACAC ACAAAAACA C

221

25

(2) INFORMATION FOR SEQ ID :932:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 333 base pairs

(B) TYPE: nucleic acid

30

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :932:

TGCTCTATTG CTATCTCCTG ATATAGGTTA TATATATATT ATGTCTTGAG

50

CGTCATGTCT TGTGCTACTA CACCGTGTTA ATCCCAGCTA CTCAGGAGGC

100

40

TGGAGGATCG CTTGAGCCCA GGAGTTCTGG GCTGTAGTGC GCTATGCCGA

150

472

TCGGGTGTCC GCACTAAGTT CGGCATCAAT ATGGTGACCT CCCGGGAGCG 200  
GGGGACCACC AGGTCTGCCT AAGGAGGGGG TGAACCGGCC CAGGTCGGAA 250  
5 ACGGAGCAGG TCAAAACTCC CGTGCTGATC ATGTAGTGGG ATCGCAGCCT 300  
GTGAATTAGC CACTGCACTC CAGCCCTGAG CAA 333

## (2) INFORMATION FOR SEQ ID :933:

10

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 281 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
15 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :933:

20

AGATTTATGG CTGCTTTCAC TTGGCTCCAT GTTCTGCTGA TAATTAAACA 50  
GTTTGTGTGT CCTGTCTTTC CTCAAAGGAA CTTGTCAACC TTTGGAATTT 100  
25 TGTTTCATCTC AGAGGGACGT CTTAAGTACT CAGCTTTCTG AATGTTTAAG 150  
AAAAAAATAA TACTTTTCAG AATTACCTAC CTCTTTCTCA TTTTTCAGCCT 200  
GGGATCAATT ATTCCCTTTC AACTTTTTTT ACATCCTAAG TAGAAATAAA 250  
30 ACTCTTTATT CTATTTTTTT TCAGTTATTG G 281

## (2) INFORMATION FOR SEQ ID :934:

35

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 266 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
40 (D) TOPOLOGY: linear

473

## (xi) SEQUENCE DESCRIPTION: SEQ ID :934:

AATCTTGTAT TATGTTAATA TTAAAATCTA ATAATAAGAT ACTGTAGAAG 50  
5 TATTTTACAT TTTTGGGGTA TAGGCACAAA TATATACATT TAAATATTAG 100  
TAATAGAATT GAACAATTAA CTATAAAATA TTATATCATA ATAAACTGTT 150  
GTTTTATCCC AAGGGTAGAG GGA CTCTAAG TAAACTGTA ACAGAATCAA 200  
10 AAGGTTACTG ATAGTTAGAA TGGGTTGAGA ACTATTTTAA CTTGGGAACT 250  
TTAAATAAGT AAATCT 266

## 15 (2) INFORMATION FOR SEQ ID :935:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 178 base pairs  
(B) TYPE: nucleic acid  
20 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## 25 (xi) SEQUENCE DESCRIPTION: SEQ ID :935:

GGAAAACAAA TGTAAGGAGG GAATTCAAAT ACCTAGTTAA TCTATTAAC 50  
ACTAATAACT CATTAAATAA ATTAATAATA TTAAATGATC TGTGTGTTCC 100  
30 ATGCAAATAA CAGAATGATT TCCACTGAAT AGTCATGATG GTTTAAAATA 150  
TTACTCTAAC ACCAATAACA ACACGTAA 178

## 35 (2) INFORMATION FOR SEQ ID :936:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 224 base pairs  
(B) TYPE: nucleic acid  
40 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

474

## (xi) SEQUENCE DESCRIPTION: SEQ ID :936:

5        ACTCAGCTCC GTGCGACCCA CATGGCCCCA GCGGGGGGA CACCAGAGGC        50  
      TCCTCCATGA GCAGCAGGAG TGAGCGGAGG AATGTGCCCC ACAGCAACTT        100  
      TCCCAGCCAA TGCCACGATG GAGATGACAA CCCAGATCT GGGGANACAG        150  
10        AAACCACTCA GAACGGCACA GGGTAACTGG CCCCAAACGC TGAAAGTTAG        200  
      ACTTCACCCG AATTACATTT ACCA        224

## (2) INFORMATION FOR SEQ ID :937:

15

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
20        (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :937:

25

      ATTTTTTTTC CCAAGAATCC CCAACTCAAT AAAACCGTGA AACAATTGCT        50  
      GGGGATGGGT AGAGAAAACC CATTTATAGT ACTTTTCTGC CTTCTTGTGG        100  
30        TTTTCGGCTT TGCGATCAGG GACTGAAGAT AGAAGGAAAA AAAAAAAAAA        150  
      AAAACAAACA CAAAAACATT TCAAAGAGA AAGGAAAAAA CTTTTTCCAA        200  
      CCAAAACCTC TAAAAAACCC AAAACAGAA CAACCAATTA AACCCGACCC        250  
35        GACACAACCT CCAATGACTG        270

## (2) INFORMATION FOR SEQ ID :938:

40

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 215 base pairs  
(B) TYPE: nucleic acid

475

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :938:

	AGCCTTCTCC CTATTCGATA AAGATGGCGA TGGCACCATC ACAACAAAGG	50
10	AACTTGGAAC TGTCATGAGG TCACTGGGTC AGAACCCAAC AGAAGCTGAA	100
	TTGCAGGATA TGATCAATGA AGTGAATGCT GACGACAATG GCACCATTGA	150
	CTTCCACAAA TCTTCAACTA TGATGCCTAG AAAAAAGAAA GATACAGATA	200
15	CTAGAACTAA AGTCA	215

(2) INFORMATION FOR SEQ ID :939:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 303 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :939:

30	TGTCGTCCTT AATATTTCTN AGCCTTTTGT CATAGAGGTG GTCGGTTGGA	50
	CCTCAAAGCC TCCATCTAAT TTTTTTTGTC TATGTTTCTA TATCTCTCTC	100
	TTTACGCTT CTTTCCCGGA CCGTCCCCTC CCTCTACAAT TATATTTACT	150
35	ACCTTCATGA TTGCTTTTTA TTATTTCTTT CACTCATCAT TATTGTTTAT	200
	TTTTTAATTA ACAATTTTTT TCATTATTCT TTTTCTTAAT TTGTAACCCG	250
40	TTTCTAATTT TCTCAATTAT TGCGCTTCT CAACCCCCCT CCTTCCTCAT	300
	TAC	303

476

## (2) INFORMATION FOR SEQ ID :940:

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 330 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :940:

ACACTATTTT CAAAATCCA AATAAAGTG CAGTTTCAGA CTTTTTAAAA 50  
15 AAACACCGTT GACCTGTCTT AGTTGTACAT TCAGAAAATG TAGCCTCGAG 100  
CGTTTGCATG CAACACTGCA TATTTTTTCT AATCAGATTA ATATGAGTTT 150  
TAATGTTTAG CATGAACTAC AGCTAAGGAT AAAAATTTTA AAGTAGCTTT 200  
20 CATAGTCTAG ATTCCTGGTT TCATAATGCT TTATGTAGTA CATTTCAGTT 250  
TGCTTTGCTT TGTGGAGACT TGC GCGTATT TTCTTTTGCT TGTTTGTTTA 300  
TCGCCAGGCA GCGCTGTTTCG AACTGTGAGA 330  
25

## (2) INFORMATION FOR SEQ ID :941:

## (i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 107 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

## (xi) SEQUENCE DESCRIPTION: SEQ ID :941:

TTTATTTTCAG ATAATTTTAT GTAAACAAAT TAAGAGTTAT TCATTCAAAT 50  
40 TTTTGGCAGT GTTAATCTGT AAATGATGAC TTGATGTACA GAAAATGCAT 100

477

TTTTGCT

107

(2) INFORMATION FOR SEQ ID :942:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 126 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :942:

15 CCACAGCATA CACACCTTGG AAACCAAGAA GACTCTTTGT GTGTGTATGT 50  
GTGCGAGACT GACGCGTCTC TACGCGCTCT ATGGGGGGAG ATTTGGTTAT 100  
TTCGGCGTTA CACCTCCGGT GTTCTC 126

20

(2) INFORMATION FOR SEQ ID :943:

- 25 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 155 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :943:

ACTGAACAGC CGCTGGTTCC AGAACAGGCA CAGAAGGCTC CAGCGCTAGA 50  
35 AACAACTGGC ACAGGAATGG TAACAATAGT CTGGCTCAGC CACAACAGGA 100  
GGCTCCGGGA CAGTCACAAC CGAGAGCTTC CAGGACAGTT ACAGTCTGTA 150  
AGCTC 155

40

(2) INFORMATION FOR SEQ ID :944:

478

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 287 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :944:

10

CGTGAGGAGC AGGTACCATT TTTAGTAGTC ACACAATTCC ACCTCCTGTT 50  
TTTACTACTG GCAACTTCTA CTTGAGAATA ATGTTCTGAA AATGGAGGTG 100  
GGGGGGGGTT TGGAAGCAAA CACATTTGGG GTTTTAAACC AATTGTTAGG 150  
TTCTTTTTTAT TTAGGGTTGT GCAGGGAAC TTTGGGAGGT TTCTTTAGGT 200  
GGGATGGGGG GACTGGGTGT TGGTTTTTGG GGGGTTTTTG GGACGGGTTT 250  
TATTTTGTCC CTTAACTTGG TTTGTTGGGC AGGTGGG 287

20

## (2) INFORMATION FOR SEQ ID :945:

25

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :946:

35

ATCATTGATC AATGATATGG TTTGGATTAC TGCCCCGCCC AAATCTCTTG 50  
TCCAATTATA ATCCCCAGCA TTGGAGGAGG GGCCCGGTGG GAGGTGATTG 100  
GATCATGGGC ATGGACTTCC CCCTTGCTGT TTTCGTGATA ATGAATTCT 149

40

## (2) INFORMATION FOR SEQ ID :946:

479

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 261 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :946:

10

TTTAAACTGC AAATAGTCGT TACAAAAAGT TTTNNNNNTT CTTTAAATA 50  
AATTCACAC AAAGAAAGAG AAATAGAAAG CGACGGTAGT GACCAGCAAG 100  
15 AGGAATAATA ATTACATTCA TCTTAATGTG TGTGTGCCAG TTCTGTTTAC 150  
ATTAACATTG GAAAACTCCA GACCTGGACA CCAGAACCTC AAATCTGTGA 200  
GTGGAATGTC TTGAGATGGG CACGCTGGAA GTCAAAGGGT TTCTCTTTTT 250  
20 TTTTTTCCC C 261

## (2) INFORMATION FOR SEQ ID :947:

25

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 264 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :947:

35

CTTTAGGAAC TGTCAGCATG TTGTTGTTGA AGTGTGGAGT TGTAACCTG 50  
CGTGGACTAT GGACAGTCAA CAATATGTAC TAAAAGTTG CACTATTGCA 100  
AAACGGGTGT ATTATCCAGG TACTCGTACA CTATTTTTTT GTACTGCTGG 150  
40 TCCTGTACCA GAAACATTTT CTTTATTGT TACTTGCTTT TTACACTTTG 200

480

TTTAGCCACT TAAATCTGC TTATGGCACA ATTTGCCTCA AAATCCATTC 250  
CAAGTTGTAT ATTT 264

5 (2) INFORMATION FOR SEQ ID :948:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 149 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :948:

CCTCGACTTA CCACGGGTGA TCCCAGAATG GACTATCAGC GGTGTTTTGA 50  
GCCAGGTGTA TTGAGCACTG GGCTCCAAC TATTGTTAAT GAGAAACGGC 100  
20 CCAACTTGGA CCATGACTTT CCCATTGCA GGTCTTAGAA TAATTTTTT 149

(2) INFORMATION FOR SEQ ID :949:

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 242 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :949:

35 CGCTCAGGGT GGAAGTGGCC GGGCGCGTCG AATGTGCCGA GCTGGTGCGA 50  
GTGGGCGAGC AGAGCGCCTT GAGGGTTGAG CATCTTCTGG ATCCAGCAGA 100  
GGCCTCCCAG GAGGGGAGCC AGGTGGCTGA AGGCAAGCAC TTTNNNNAGG 150  
40 TTCTAGTCCC CTTTTTAGAT CCTAGGGGAC TGGAGATTG GCACCTTCCC 200

481

CCAAGGCTTG GCCTCGTGCC CTATAGGGTG CCCCCCTCTC TT

242

(2) INFORMATION FOR SEQ ID :950:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 153 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :950:

15 ACTCTGCCTG CACTATAAAA TGAACCAAGG AGGATCCAGT TTGCTGTCTG 50  
CACTGACAGA TTTACAGACA GGAAAACAAA GCCTTACTTA CCAGGAATCC 100  
AAAGTTTATA CATGAAAATT TAAAAGGGA GTCTATGCAA AGCGGAGTTC 150  
20 AGG 153

(2) INFORMATION FOR SEQ ID :951:

- 25 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 128 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :951:

35 TGCGGGAGTC TCACTGGGGG GGGGACACCT GTGCAAACGC GTAACGCAGG 50  
TTGTTCCCTAA GGCGAGCTCA GGGAGGATAC AGAAAACCTCT CCTGTGGTGC 100  
TATGAAATGT GGCGTAAAAA GCATTCTG 128

40

(2) INFORMATION FOR SEQ ID :952:

482

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
5 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :952:

10 GTTGGAAATT TCCCTCAAAT CACCTACCGA TTACCCTTGA TTTCCCTTTG 50  
TTTTCAAGTT CTCAAAACGA ATGAAATAGA ATATAGCAGA ATGTTAACCC 100  
15 ATATAAAAAT AAAGTGTACC CAAATATTGT AATGTATATT GCTGCTCTTC 150  
TTCAAATTAA ATAAGGGTTT AAAACCACTT AATTGGTAAT ACAACATCTC 200  
AATTGATACA AAT 213

## (2) INFORMATION FOR SEQ ID :953:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 236 base pairs  
25 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :953:

GCAGCAGTTT CTTTGAAAAT TTGGACCAGA AGGTGCATAA CAAGTTGTTC 50  
35 TGCAGAAGTT CTTATCTGAT ATTCTTAGGG AGCTATCCTG CATGTAATCT 100  
TCATTATTTT TTTTCTCTAC CATCATGTAG GCATACTCAG TGTAAGACTAC 150  
CACAATCCTG GATACCTCTC TGCTTAGATT TACAATCTCT GCTAAGATTT 200  
40 GCCACTGCAG AAAGTGTAGT ATTTTCACTA CATTAT 236

483

## (2) INFORMATION FOR SEQ ID :954:

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 217 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :954:

GCAGCAGTTT CTTTGAAAAT TTGACCAGA AGGTGCATAA CAAGTTGTTC 50  
15 TGCAGAAGTT CTTATCTGAT ATTCTTAGGG AGCTATCCTG CATGTAATCT 100  
TCATTTTTTT TTTCTCTACC ATCATGTGAG GCATACCCAG TGTAGACAAC 150  
CACAATCCTG GAAACCTCTC TGCTTAGATT TACAATCTCT GCAAAGATTT 200  
20 GCCACTGCAG AAAGTGT 217

## (2) INFORMATION FOR SEQ ID :955:

- 25 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 256 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
30 (D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :955:

35 AGCAGCGACC GCGCTCACTG GCTTTTTGTT TCTGCTTGGG CCTTTTCTGT 50  
TCAGTCCATG CTTGAACTAC TCCACCCCCT TAAATCCAAC GTAAAAACCA 100  
GTCTTTTCTG TGCTTGTTCT CTGTGCGTTA ATGCTTTTTC TTATGCTTGC 150  
40 TTATTGAAAT ACTGTATTTT CATTGTCCCC TGGCCAAAAC ATCTGAGTCG 200

484

TGAAACCATT TTAGATACTC TACTTTCTTA CTGTGTTACG TGGCATTTTA 250  
TGCTTG 256

5 (2) INFORMATION FOR SEQ ID :956:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 194 base pairs  
(B) TYPE: nucleic acid  
10 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :956:

CAAGCAATTG AGAGACTTTT TTCCTGTTAT TTTTCTACCA TTTATTTCTC 50  
ATTTCAATTAT ATTATGGTCA GAGAATATAT TTTGAATGAT TTCATTTATT 100  
20 AATTTTAAAA AATAACATTA AAAAATTTTT TAAAATGTGA ATATACCACA 150  
ATACAGTATA AAGATTGTAC ATTCTGTTTT TGGACAGTTT TCTA 194

25 (2) INFORMATION FOR SEQ ID :957:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 196 base pairs  
(B) TYPE: nucleic acid  
30 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :957:

ATCTATTTTT CTTGGTCTCA TACTCAGTTT TTTATGTAGT CACTTAGTAA 50  
ATAACCTAAA AAAACATGTT TTCTCCACAC TAATTTTAGG GTGAATTCCT 100  
40 CATTTGCTT TTCAGATCAT GGGGTGAGGG GGATGGTTTCG TGTGTGTGAG 150

485

GAACTGAGGA ATCAGATGGA AAACAATGCC TCTGCTCCTT TGAGTA

196

(2) INFORMATION FOR SEQ ID :958:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 105 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :958:

15 GCGCTCAGCT GGAAGTTCCG ATCTATTTTT TCTTGGTCTC ATACTCAGTT 50  
TTTTTATGTA GTCAGTTAGT AAAATAAACC TAAAAAAAAA CATTGATTTT 100  
TTCTG 105

20

(2) INFORMATION FOR SEQ ID :959:

- 25 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 261 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :959:

GACAGCGACC GAACTCAAT GGAATCCCGA TTCCATGGAA ATGGAAAATA 50  
35 GCTCTATTTA TACAGCAAAT TCAAATACAG TAGCTTGCTA AGCAACTTCA 100  
TAATTCATTA AACTCGATG GCAGAGCAGA TAGTCACAAT TACTAACGAT 150  
TATCATGATC TGCATTCTTG ACAAGTATAC TATGGCGAGA TAAATCAAAC 200  
40 TCAGACGATG ATAAGCAAAC TCAAAAATGA AAATGATGAT GCCAACTAAG 250

486

CTTTTGTTAA A

261

## (2) INFORMATION FOR SEQ ID :960:

5

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 188 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :960:

15

CACAGTTTTG TTGACTAAAC TCTACAGAAG TCAGGTATTG GGAAGGAGAA

50

TCGTTTCTTC TTTAGAGGAG TAGGTTTTAA CCATGTTAAA TTTCCAAGAA

100

TAAATTTATT TATCACCTCT ACACAGCGCA GACCATTTC AAAAAATAAA

150

20

TAATTTTCGA TTCAAGTACT ATACAACTT AACGATGG

188

## (2) INFORMATION FOR SEQ ID :961:

25

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 191 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :961:

35

ACTTTCGCCT ACCCGGAGAG GCCCAGAAAA TTGACCAGAT GATGGAGGCC

50

TTCACCCAGC AATACTGCCT ATGCAACCCT GGAGCTTTTC AATCCACAGA

100

CACACGCTAT GCACTGTCCT TCGCCATCAT AACGCTCAAC ACCAATTTCT

150

40

ACAACCAAAA AGCCAGAGAC AAACCTGACC TAAAGCGCTC C

191

487

## (2) INFORMATION FOR SEQ ID :962:

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 191 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :962:

CCAAGGCAGA GTTTATTAGG TTTATGCTTT ATATTTATAT ATAAGGTTTT 50  
15 ATTCATGTTA AAAACTTAAA ACCAACGGAT TATGCAAAGT GATAAGTGTA 100  
TCAATGAATA TACAACTGAC TGGATTTTAA ATATACACAA ACCAGTATAC 150  
CCCCAGTACT TAAATGAAGG CACTCAGTAT ACACCAAAT T 191

20

## (2) INFORMATION FOR SEQ ID :963:

## (i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 178 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :963:

AGCAGGCCAA AAGCCCAGGT GAGGCCAGC AGGAACAGCA GCCCAATGCC 50  
35 TCCTAGCACT CAAGATCCAC CATAGTCCAA GCAACTGCAG TTACACTTGA 100  
GTACAAATAC GCTCCCGACA GCCTCATGCA GCGACACCCT AAAGGACACC 150  
CGAACACCAT CAATAACCGA ATAGACTA 178

40

## (2) INFORMATION FOR SEQ ID :964:

488

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 199 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :964:

10

ACTTTGCAGT CCTCACATCA CAAATAGAGT AAAAGATTCC CAAAAGGAAG 50

GGGATCCTTT TGACTGCCAG ACGCGGGAAG GAAAGAATGA AATTAAAGAA 100

15 TATCCTTTTA AACACACACC TCGACACAAT TTTCCACTCT GCTAAGGGAT 150

CACAAAGACT AAGACGCGGG CAGACTCCCC ATAAGCCACG CTTATAACC 199

## (2) INFORMATION FOR SEQ ID :965:

20

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 217 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID :966:

30

ATGGAGCAGG ACCTGCGATG TTCTGATGGA TTATACCCAC AGTGATTTTT 50

GGCACATCTG CCAAAGCTA CAAACAACCC CTAATAATTA CACACTACAG 100

35 ATAGTGAGAA GCGTCCTACC CAGGAGTCCT GAATGTGATC TGAGTATGCT 150

CTAAGGCAGC CCCAGGAAAA GCAATCCAAT CCCTTTCTCC TCGCCTTTAA 200

ACCTGCAGGT TGGGGCT 217

40

## (2) INFORMATION FOR SEQ ID :966:

489

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 175 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :966:

10

ATTTGCGACC AAAATCATCT GGGTTTATAT TTGAAAAAAC CTTGTTTTCC 50  
AATTAAAAA TGCCAAGAAA GTTGTGAATA CCGTTCATTA TCACTAGGAT 100  
CAAGAAAAAG CAAATGGTTT AAGTTTTTAC ATAGGAAATC TAAGAACTAC 150  
TCATCAATAA AACGCAACAC TATCA 175

## (2) INFORMATION FOR SEQ ID :967:

20

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 92 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID :967:

30

AGGGGTTTCAG GCCTGGAGTC AGGGAAGAAG GGGAAAGGGG CAGATAGCTG 50  
GGGGACAAGG AAAACCTGGC GGGGGGACCC GCGAAAAACA CA 92

35

## (2) INFORMATION FOR SEQ ID :968:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 208 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: lin ar

40

490

## (xi) SEQUENCE DESCRIPTION: SEQ ID :968:

5           GTAATATTAG GGACATGAAT GTTAGTACAG TAATTACCAC ACATGGAAAA           50  
          TATTGTTTCA CAGGAAAAGT AAAACTTTCA AAAAATTCCC TAAAGATCCT           100  
          ATTCAATAAA CAATTTTAGA TTTAAGGAAC CACTTACGCA AACTCGAAC           150  
10          AAATAACCGA AACTCCACC TACCGCGCAA TACTCAAAAA CACAAAAATA           200  
          CTACTAAC   208

## (2) INFORMATION FOR SEQ ID :969:

15

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 256 base pairs  
          (B) TYPE: nucleic acid  
          (C) STRANDEDNESS: double  
20          (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :969:

25

          AGTGGTTGGT GTTACTGGA ATCTTGTTTT TTTTTTTTCG GTTTTTTTGA           50  
          CTACTCGGGG GGTTTTCCTT TTTTACAGGA ACTAAATCAA CAAACTTTTT           100  
30          CGATTCCTCA ACTTTAGATT TTTATTTTTT TTGATTACCA TTTACTTTTC           150  
          TTCATTTAAA ACTTTTAACG CCTCAGCCTT TTTCTTAGGC CAAGGCCTTC           200  
          CACCAAGGAT TTACTCCGGG ACGGATCTAA CTGGATTTTC CGAGGTGGGT           250  
35          TTAAGA   256

## (2) INFORMATION FOR SEQ ID :970:

40

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 240 base pairs  
          (B) TYPE: nucleic acid

491

- (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :970:

	AATCTATTTT CCTTGGTCTC ATACTAAGTT TTTTATGTAG TCACTTAGTA	50
10	AATAACCTAA CCCGCTTGTT TTTTCCACAC TAATACTAGG GCGAATTCCT	100
	CATTTTATTT TTAAGATCAT GGGGCGAGGG AGATGATCGC GAGCACGAGG	150
	ACCTAAGACA TCAGATGAAA AACAATGCCT CTATTCCTTC AAGTATAATA	200
15	AATGATACCC GAGAGTAAAG AGCTACACTT CGCACCTCTA	240

(2) INFORMATION FOR SEQ ID :971:

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 184 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :971:

30	ATCTATTTTT CTTGGTCTCA TACTCAGTTT TTTATGTAGT CACTTAGTAA	50
	ATAACCTAAT CCGCTTGTTT TCTCCACACT AATCCGAGGG TGAATTCCTA	100
	ATCTAGCTTT TCAGATCATG GGACGAGGGA AATGACCGCG TGCGCGAGGC	150
35	CCTAAGGAAT AACATAGAAA ACACCGCCTC TGCT	184

(2) INFORMATION FOR SEQ ID :972:

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 234 base pairs  
(B) TYPE: nucleic acid

492

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :972:

	GTGTTCTCTA AGGTGATACC TTTTAATTTT GAAAGACTAA ATAATTTTAA	50
10	TCGAGAATTT CCAGTCTTTC AGTCTGATCT ATTTAATTCA CTACTTGTTA	100
	CATAATCCAG TGAAAACTCT ACTTGTTGAA ATTATGACAT AAAGATCTTG	150
	CAGCTTTATT TGAGTATTTG TTCTTTTGTG TAGTTTCCAT CTTTAAAAT	200
15	ATTTAAAATA TTTTCAAGGA TAAAGTATT ATCT	234

(2) INFORMATION FOR SEQ ID :973:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 197 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :973:

30	TTTTCATCTA AAGGAGAGAG GCAGGCTCAG CTCCTGAAGG TCGCAGAGCC	50
	TCAGTAGTCC TCCTGAGTGC GTCTAACTAA CTACCATCAA AAAACAAACA	100
	AAAAAAACAT CACAAAACCTG AACTGCCGCC ATCACCCTA CACCAAGTAT	150
35	GTGATTGAAT TATTCAATGA TCTGTTTTCG CGGTAGTGAC CAACANC	197

(2) INFORMATION FOR SEQ ID :974:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 244 base pairs  
(B) TYPE: nucleic acid

493

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :974:

	AGCAGGAGAT TTTTTTAATA ATAAACANCA ATGGAGAGGT GGAAATAGAG	50
10	ATGGAAAAAC AGGATCAAAG GAGCAACATA TCCAGTGA CT TAAAAAATA	100
	ATCACACGTG GCAAGAAGTT TTCTAAAGTA AACTGTATGT GGGGAGAAGC	150
	ATACAGAAAA AACGAAATA CATAACCCCC CAGGTTTGAA AGAAAATAAT	200
15	TTTGAGTTGT ATCAATCTAT CGATATCAAA GAATGAATGA CCGC	244

(2) INFORMATION FOR SEQ ID :975:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 330 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :975:

30	TTTTTTTTTC TGAACACTTT GCTTCACACC TTCTCATATT CACGGTTATG	50
	AATTCTCCTG ACTATATCTA TTGTAACCCA AACAGCAGA CTGTATTTAG	100
	AGACCCATTA GAGATTTTCAT GTCTATATGC CCAGAGCCTG ATATAATGCC	150
35	ACCTTACTAT ACACATAATA TAGAATCTGA GGACTACGTT AACTGATACA	200
	TGTTAAGTAT CCTGCAGAGA GCTGGCACAT TGAATGTGCT CAATAATCGT	250
40	TAGCTTTAAG TATCTACCTC AAAGGGCTAC TGTGTGACTC CAATGAGATA	300
	ATGTGCAATG AAGGGTTTCG TGTAATATTG	330

494

## (2) INFORMATION FOR SEQ ID :976:

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 200 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :976:

TGGTGAAAGG AATAAGCAAC TCAAGGTAAA TAAAGAAGAA AGATGAAGAT 50  
15 TCTTAGAATC GTAGAAAGAC TGCAGGGGGA AATAATTAAA GCAGCTTTAT 100  
TCCTTACGGC ATTCATCATT CGTCGAGCTG GAAAGCACTG ACAACTTTGT 150  
AATGAGTTTT TTGCGCTTAA CTCTGTCAGG TGATTTATAT GAATNACTTA 200

20

## (2) INFORMATION FOR SEQ ID :977:

## (i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 296 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :977:

AAAGGACAAT TTAATATAAA TCTATGTTTG TGCATTTCTG ACAGGCCATT 50  
35 ATTATCTGCT TTGACAAAGC CTTTCTGAAA CGCAGTGTAC AATGAATCTT 100  
AATGATGTTA TGAAACGAGC TTTGCT 3 GCTCTTGATT GGAGCTTCCG 150  
GTATGTGATG ACGGTATGTC ATGTATGCAT GGATGTAC 3 AACTGTGTTT 200  
40 AATACTCTGA ATTTTAATTA GAAAAAATA CAATAGCAGC AAGGCCCTGG 250



495

TTTCTAAGCT GCATACTTTT ACTAACGCGG GACATGAGCA AATGCC

296

(2) INFORMATION FOR SEQ ID :978:

5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 228 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :978:

15

GAATCNCGCC TGACACATAG AATGCATAAA CGAGGGGGGT CCTTCTGCAG

50

ATACTCTAAT CACTACACAG CTTTCTCTAT AAAACTACCC ATAAGCCTTT

100

AACCTTTAGA GAAAAATGAA AAAGGTTAAT GCTTGGAAGC CGGGGGAGGA

150

20

CTGACCACTT CATAAGCCAG TACGTCTGAG CTGAGTATGC CCCCAGAATC

200

CAGCCACTAC TGATAATTCA CAACGGTA

228

25

(2) INFORMATION FOR SEQ ID :979:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 171 base pairs

(B) TYPE: nucleic acid

30

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :979:

CGTACAAAAG CGCTTTGGAG ATGCCAGAAA AAACCCTACG GGAGGGTTAT

50

CCCCCTGACG CTAGGCCATG ACACAACTAA ACTTCAATAC ACCAGGACTA

100

40

AGGCAAGTAT GAAGAAGCAA AATATCGTAA CGACGCACCC TCGAGATCTA

150

496

CCAGGCAAAA CCAGAACCTG A

171

(2) INFORMATION FOR SEQ ID :980:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 241 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
10 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :980:

15 TGATTCCCA TTTCCCTGGA CAGGGCAGAG TCAAGCCGAG AAGGAGGAGC 50  
CACAGGCCAG CTGTTAATGA GACACTAAAT AAAACGTTCA GTATTCATAC 100  
CTGTGGAACA TGGGTGAACC TTTCTGGTAA CTCGATTTTT CACACCAATG 150  
20 ACAGCAAATG AGAAAGTGAG AGAAGCTAGA TAAATGTTTT TAAAGCATT A 200  
CTGCAGTGGA AAATAACTGC ACTCTCAGGA CACAGCACTG T 241

25 (2) INFORMATION FOR SEQ ID :981:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 227 base pairs  
(B) TYPE: nucleic acid  
30 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :981:

TCACTGCAAT CACGGTAGCT TCGCCCAT TG CCTCTTCAAC CAGGCACATA 50  
CATCGAGAAG TTGAACCTGC ACTTTATTTC AACTGAACA GACTTACCCC 100  
40 GACAACAACA CCTCCCCAGT GGGACAAACC TACCCACCT CCCCACACTC 150

497

TACTCCCAGC TAACGTTCCC TATAATCATC ATGACCCATT AACATTTGC 200  
AAAACCACAC TTCAACCCAC AGGAAGA 227

5 (2) INFORMATION FOR SEQ ID :982:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 205 base pairs  
(B) TYPE: nucleic acid  
10 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :982:

CGTTGTCGCC ATGGTAATAC CGCTCAGTAC GGGAGGACCC ACAGGCTAAG 50  
ACACTCGGAG CACGAGCTCG CCTGAGGGAC CAACGAGGCG AAGCCACAAT 100  
20 CCGCGAACTC ATGACTGACC CCTTCTAAGT AAGAATCCCA CCCAGGCAAA 150  
CCAATCCGAC AACCGAAATA GCGCAGGCAC CGCCAAATTC AAGGCGCCCC 200  
25 AAAAG 205

(2) INFORMATION FOR SEQ ID :983:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 204 base pairs  
30 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :983:

AGCAACCGGC ACTCAAGTGG AATCCCGAAA AAGTGATTTA AAAATGATCT 50  
40 TACCTGTACC AGAAAAGCAA AATTAAAGGA AACAAAATAA GAACCATAGT 100

498

CCCAAATGAC ATTTAACCGT ACATACAGCG ATAACATGTT CAAAATCCAA 150  
CAAATAACGC AACTTCCAGA CGTAAATATC CGCCACTCGA TTCCCTCCCC 200  
5 CCCT 204

(2) INFORMATION FOR SEQ ID :984:

(i) SEQUENCE CHARACTERISTICS:  
10 (A) LENGTH: 168 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :984:

ATTTGTATTA GAAAAGTAAA GTTGAAGGAA ATAAAATTG CATTCTTGTT 50  
20 TTAAGTGATC TTTAATTGTA TATATCGCGG TAGTATGTTC AAAATCCACT 100  
AAGTACTGTG ACTTTTAGCT GCAAATCTTT GCTCTTTGCT TTTTTTTTTC 150  
25 TTTCTCCCCC CTCCCCAG 168

(2) INFORMATION FOR SEQ ID :985:

(i) SEQUENCE CHARACTERISTICS:  
30 (A) LENGTH: 350 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :985:

CTCAGCTGGA ATGTCCGGTG CCTGCTAGGT GCATGGCCAG AGAAGCATGG 50  
40 GCTGGGCCTG GGCACAGGAG GAGCAGCTGC TTTGGTCGGG GTGGAGACTT 100

499

TTTTTTTTTT TCTACCCACA GCCTATTCCA CTCCTCCCCA TCTCCAGGCG 150  
CTGGGAGGGG GGCCCTCACC CCGTCACGCC TCGCTCCCTC CTGGCCCTCT 200  
5 GGTCCAGCCC CTTACGCCTC CTCTCAGTCT ACTCAATTGT GACTGTCCCT 250  
CCTGATGTAT TTTTTTTTCC TCCAAC TAA AAGGCAAAAA TAATCCTATT 300  
TTTATTATCT TGCTACAAC TCAACTTTCT GCCCTATAAA TTTACATTCC 350

10

(2) INFORMATION FOR SEQ ID :986:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 289 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :986:

AGCGACCGCC ACTCACTGTG AGTTCCACTT AATTCAGGTG AGCCGCTCTT 50  
25 CTGCACCTCC TCCTCACACC TCTCTACCTA TACTAACCAT TTTGAAGGT 100  
TCAACAATGC TCTGCAAATC TTTTAAAGAC CCGTTACTTC AACAACTCCC 150  
AATACCTTCC TCCTCAACGG AACAACTTAA CCGTTACCTT TTAAACCCGA 200  
30 CGAGCTACAA AGCAAGAGAT ACTTCGCGAG CCAAATTCTA CAAAGGACCA 250  
AAAAAGAAAC CCATTACCTT ATAGTACTCA TGCAAAAAA 289

35

(2) INFORMATION FOR SEQ ID :987:

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 134 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

500

## (xi) SEQUENCE DESCRIPTION: SEQ ID :987:

5 CACAATCATA GCATTTATTA CACGATTTAC ATCTGATCCT CACGCAATTT 50  
TCTTCCTCAC CAATAAAGAA CTAATAGGAC AGCATATTAG AAGCAACATA 100  
CATTCTTTTA TTCTTGCATC GCTATAAAGA AGTA 134

## 10 (2) INFORMATION FOR SEQ ID :988:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 287 base pairs  
(B) TYPE: nucleic acid  
15 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## 20 (xi) SEQUENCE DESCRIPTION: SEQ ID :988:

TTCTGAAATG AAGGTTTCGT CTTTAGCTAT TGA CTGTAGG ATTTGTAATT 50  
CAAATCATCA CAGCATCCTA AAGAAATACT GTGTGAATGG AATGCACACA 100  
25 ATTCCTACAG AACACACAAA CTGATGTCCA AAAGGCACAG AGTAATGCTG 150  
GTGGCTCTTT CTAGTCAGTT AAGAAACAAT AAAAAGTCTG CATTATTCTT 200  
30 TCATAATTTA AATACTTAAG TAATCTCCAC TTTATTATTT TATAACAATG 250  
ACTTCAAATT TACATTATTT TAAGTACCAT TGTAATC 287

## (2) INFORMATION FOR SEQ ID :989:

35

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 177 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
40 (D) TOPOLOGY: linear

501

(xi) SEQUENCE DESCRIPTION: SEQ ID :989:

AGCAACCAAC ACTCACTGGA ATCCCGCAAT CAAGAGCTAA AAGGACTTCT 50  
5 TCCATCTCTC AGGGACACAC ATCCACCGAT AAGAATAAAA GAAATGCCTG 100  
AATGACTCTC ACTGGCACTT TTAACACAG CAAGCCCAAC ATATTTTCTC 150  
CTTTTCATAA AGAAGCCTAT ACACCAT 177

10

(2) INFORMATION FOR SEQ ID :990:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 158 base pairs  
15 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :990:

TTCCTATACT ATGTCGGTTA AAAGCCTTCA TAGAATATAG GCACCAAAAA 50  
25 TAAACTAACC CCACACCCTC ACCAACCAAA GGAGGCACAA TCCAACGAAA 100  
CTGATGAAAA GTCGAGGTAA CGACTCTGCA GACCGTACTC ATTTCTAAAC 150  
CAAAAGTC 158

30

(2) INFORMATION FOR SEQ ID :991:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 267 base pairs  
35 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :991:

502

TAATCCCTTT TAAGCAGAGA TACAC TTCA CAGAGAGAGA ATGTTTTAAA 50  
AAGACCCACA AGGGGAAGGG ACCAAGTAAG CACTTTTAAT TCATTTTGAT 100  
5 TACACAAAAA TAAGGCAAAC TAAATGATTC AGAACAATTC AATTTAACTG 150  
AAGCCTTCTA GAAAATACT CAACAGGCTT CAACAAAAAG ACTTAGCGCA 200  
CATAAAACAA TCACGAAGAT CACAATTTCA GCACAAATAT CTGAAGGAAT 250  
10 ACACGCAAAA CATCATA 267

(2) INFORMATION FOR SEQ ID :992:

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 199 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :992:

25 AGGATGTGTT CATGCTGGCT TTCAGGATGT CCCAAGGCAC GGCACACTGA 50  
TTGTCAAATT CCACTTTGCA TGGAAGACAG CACAGAACCC TGCTCTGCGT 100  
CAGCTGGAGA GCTCCGGCCA GCACGGCCAC CAGCAGCATG ATCAGTGTGA 150  
30 TGCAATACCA GAAGCCGTCC CACCATGATT TTAAGATGTG ATAAGATGA 199

(2) INFORMATION FOR SEQ ID :993:

35 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 198 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40

503

(xi) SEQUENCE DESCRIPTION: SEQ ID :993:

TTTAAGGTGC TAAACTTGCA CCTCATGTCC ACTCAGTAAC AAGTATTGGG 50  
5 ACGTAGAGCA CAGCCTCACT CAGCTCTGAA AGGTAATACA GCTTGCGAGG 100  
AAGTGAGCCA GCAGTGGCCT TTGCAATTGT GGATCTTGAG CTTTGCTCTT 150  
AGCAGATCTC AGGCGTAACC ATTCGCTAAC TGTACTGAAG ATGCGTCC 198

10

(2) INFORMATION FOR SEQ ID :994:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 183 base pairs  
15 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :994:

GCTATCTGCG GGGCCATTCG TAGGATGGGT GAGTCAGATG ATTCCATTCT 50  
25 CCGATTGACC AAGGCCGATG GCATCGTCTC AAAGAACTTT TGA CTGGAGA 100  
GAATAACAGA CGTGGAATAT TTGTCATAAA TAAATAACGA AAACCTAAAA 150  
AAAAAAAAA ACAACA AACC CCAACAAACT CAA 183

30

(2) INFORMATION FOR SEQ ID :995:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 199 base pairs  
35 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :995:

504

ACCTCTGCAT TAACACTCCA GCACCTTTGG TTAGCCAATT TGGCCTTATT 50  
TGTGTCTCCA CCATTGGATT ATCTGTCCAT CAAGGTCAGG AATGTTTTTCG 100  
5 GGTACCCCCA CTGTCCCCAA CTTCGAATAT GCTCACTGCC TGGAAAATGT 150  
TTATCTGAAT ATAAGGCATC AAGCCAGAAC TTGCCCAAAA CTAAATCTA 199

(2) INFORMATION FOR SEQ ID :996:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 177 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

15

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :996:

20

GGTCTTGGCT GGTGGTTTAT GGCCCGGGCC TTCTTTCTAC GGGGGCCAGG 50  
GTCCAATTTT CCACCTGGGG TTAAAAGTT AAGGAGGACC AGCCTGGGAA 100  
25 CCCCTCGAGT GGGGACGCCA TTTCTATTAC CAGGGCCCCC TTATATTTTA 150  
AGGGGACACC ATATGGAGAT TTTATGC 177

(2) INFORMATION FOR SEQ ID :997:

30

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 229 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

35

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :997:

40

GAGTTTCCTG TGCTGTTACA AATGTAACAT TCTCATATAC AACATTCATT 50

505

GAAGAGGCAC AATTCTTATT TTGAGGTGGC ACAGATTAGA CAAATTTTTC 100  
AGTGAATAAT TCCTCTTTCA TTAGGAAATT TAACCACAAG CTGTATTTTC 150  
5 GTAGAAAGTT GCTTGAAATT CTTTTCCTAA AAAAATTTAA TTTTCTATC 200  
TCAAAATGAC CGTATGCAAA CGAACATTA 229

## (2) INFORMATION FOR SEQ ID :998:

10

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 233 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
15 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :998:

20

TTGCAGTGTT TATGCCCGCC TTCTTTCACG GGCAGGTTCA ATTTCACTGG 50  
TTTAAAAGTA AGAGACAGGC TGAACCCTTC GTGGAGCCAT TTCATTACAG 100  
25 GTCCCTTAAT TTAAGGAACA AGTTGATTTA TGCTACCTTT TTGCACGGTT 150  
TAGGGTACCG CGGCCGTTAA ACATGTGTTC ACTGGGCCAG GCGGTGCCTC 200  
TTAATATCCG GGGATGTCCA GAAGGGGAGT TTT 233

30

## (2) INFORMATION FOR SEQ ID :999:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 216 base pairs  
35 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

## (xi) SEQUENCE DESCRIPTION: SEQ ID :999:

506

TCAAAAACCTC AATATAATAT GTAAATCAGG GGTGTCCAAT CTTTGGCTT 50  
CCCTAGGCCA TACTGGTGTT AGGCCACATT CAAAGCTATC CTAGGCCACA 100  
5 TGTGGCTGGT GGGCCATGGG TTGGACAAGC TTGATGTAAA TAAACCACC 150  
AGTGGAAGA GTTGTGTG AGTTACATTC AAATACAACA GGAGTAATAC 200  
TATCATGATA TTAGTT 216

10

(2) INFORMATION FOR SEQ ID :1000:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 280 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :1000:

GACAAGACCT AGAAGCAACA ATGCCAGTA GAAACAAACA CACCTACTGC 50  
CTGGATCTTA GTTTTAATT ATATCCCCA ATAAAGAGAC CCAGGGCTCC 100  
25 TTGTTGAAAT GGCTGATTCT AGGACTGGGG CAGGAAATAT GCAAGATGAA 150  
CCTAGAATAT CTAATACTGC CAAAATTAA GAAAGTGTTT TAAAAAAAT 200  
30 CCCCACGGAT AGGGTGTCAA AAGAGACATA GAAGCCATCT GAAGGAGTTC 250  
CCAATGGCCA AAGATCAAAT AATTTTCAA 280

35

(2) INFORMATION FOR SEQ ID :1001:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 324 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

507

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1001:

5	TGCATGATAG GAGCGTCCTT TGTTCTCATG AGGTGACTCT TGGTGGGCTC	50
	CTTATTTGGG GACTGGTCAC CAAAAATACC TAACTATGGT TGAAGCTTA	100
	GTGCTTTCAG CCCCATTTCCC CATCCTCTGG AAAGGGGAGC AGAGCTGGAG	150
10	CTCGATCATG CCTGCGTGAC AAAGCCTCCA GAAAAATCCT TGAAAGACAG	200
	GACATGGAGA GGCTGCTGGG TTGGCGAACA CAGCCATGTG CCGGGAGGAT	250
	GGTGCACCCC AACTCCACAA GGACCCTTCC AGACCTCACC TGTGTATCTC	300
15	TTCATCTGGC TGTCATTTG TATC	324

## (2) INFORMATION FOR SEQ ID :1002:

20	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 254 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1002:

30	ATTTCCATTC ATAAGTCCTC ACAAACCCAC TTTTCCTCTT GCCTGAGTGC	50
	CTCACATACC CTACTGCCTG AGATGGTTCC AGAGGCGGTC TCCTCTCTCC	100
	CCCAACGAAA CACCAGGCAC ACACCTGCCC CCAGTCTTGC CTGCACTCTC	150
35	CTTTCCTCCC GCAGAGAGGC ATTCCTTTCT CCTCCTCTCA TCCTACACAC	200
	ACTATAAGAG ACAACTGAAA TCTTGCCTCC TCCAGCAAGC TTCTTAATTC	250
40	ATTT	254

## (2) INFORMATION FOR SEQ ID :1003:

508

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 265 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1003:

10

AAGGTTGCGC TGCCCATCCT CTCGCCCTTC GGAATTTACC CCTGGCCGCT 50  
CAGGGTCTCG CTTCTAGAAG AAGATGATGG ATACTAGGGC GATCCTCCTA 100  
TTGCCTTTAT ATTTAACAGG CCCGCCGAGG AGGGGCTCCC GCTGGTGCCC 150  
ACATAACTCT ATTAGACCAT CTGAGGCGAC TTCCCCCACC CCCTCCAACG 200  
CGCCTCACGC ACGACTCTAG CAAAAGACAG GTTCCGCGGT GGTACGTCG 250  
TTTGAGACTA TACTG 265

20

## (2) INFORMATION FOR SEQ ID :1004:

25

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 263 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1004:

35

AAATATGCCC TGAGGATTAT CTGATGTGGA TGGTGTGGAA AAGAACTCCA 50  
GCAGGCGACT TCGAATTCAA TCAATGTCCC CTGAATGCCA CAGAACCACT 100  
AGCAGACGCT GCTCTCTCAG TCTTAATGGA GTGGCCTTCT GGGAACAGCC 150  
GAGCTTTGAA AGATGCATAT CAAATGAGTA CAGACACTTG TAGCATTTAA 200

40

509

TCAAAGAGCA CCTTGCTAAG AGGCAGCGAA TGCTGGCAGG TGATGGAATG 250  
CCCCAGGTGA CCA 263

5 (2) INFORMATION FOR SEQ ID :1005:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 317 base pairs  
(B) TYPE: nucleic acid  
10 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :1005:

CGAGACTGCA GTACTTCTAG AAAGTTGTGA ACTTCTAAGA AAGAGCCAGG 50  
CTTCCATCTC ACTATTCCTT GATCATTATC TCTGAAGTCC CTACCTGCAC 100  
20 TTCCCTGATT GTCCTGTAGC AACACCAGCA TGGTGGGAAT TGCAGGCAAA 150  
GATTGTGAAA AATCCCTAAA GGGTCATTGC TCATGACGTT ATTTCGAATT 200  
25 GTAAAATCGT GAGCCACTCA TATTCAAAC TAAAAAGAA CAGAACTTTT 250  
ATTCACGTTG TGAAGCTTAC TCCCTCGCCA TTTTACGGAT CAATGTCAAA 300  
CGCTTGCATT CATAAAG 317

30

(2) INFORMATION FOR SEQ ID :1006:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 287 base pairs  
35 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :1006:

510

	CGGAAGCATT ATCCTGTCAT CAGAAGATGG ACCTTTCCTT GGAATGCCTT	50
	TTCCCTATCA TGTCTGTGTG GTAAATACCT ATTCATCCTT AACAACTAG	100
5	CTGAGGTCTT ACCTCATCAG GATTTGATCC CCCAAAAAGA TTTGTCCCTC	150
	TCTGAGCTAT CTTTATAACT AGTACATACT CCTACCAGCG GACTATGTTA	200
	TAATAATGTG GCTATATGCC TGTGATCTCA GCGTGAGCTC TTTGAGGACA	250
10	GAGTCTTTGT CTAAATACTC AAAACCCTGT TTACCAT	287

(2) INFORMATION FOR SEQ ID :1007:

15	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 273 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :1007:

25	GGGCACCAAA ATACACATCA GAGGAGACTG GCTTCCATGA GACGCTTCGA	50
	CTGTCTCATC GGGGCACTTG TAATAAGCAT CTTGATGCCA CTGAATGCAA	100
	TGCTGTATTG AAATAATAGC TTTCATCTTC ACTATAAAAC AATACAAACG	150
30	TAAACTTTGA AGCCCTTTGA AGGACCTAAC CAAACAACAC AAGGATGAAA	200
	ATAGATCAGT ACAACTTTGA GACACATTAT TAGGTCAAAT CTGCAAAGCA	250
35	TATTCGGATT TTACCGTAAG GAA	273

(2) INFORMATION FOR SEQ ID :1008:

40	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 308 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double

511

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :1008:

10 TAGAGTGGGG GGCCAAAACC TCTGCAGTCC CCGGCAGTGA GCTATGGACT 50  
TTCTTCCCCC TCACAAGGCT GGGGGCCTCC TGCTCTCGTC CCTGGCCCTC 100  
CCTGCACAGG GCAAAGCCAG TCTGGGCTAT GGCACACAGA GTTCATGTTT 150  
GCGCCCTCTC CCTGCCCCCTC ACCCCAGAGG GTGAGGAGGA ATGAGGGGCA 200  
15 TTGATGGTTA GGCCGGTTGT TGCCTCGAAC AGCTGGAGGG AAGCTGCAGG 250  
GGTGATAAAA TCAAAGCGAT ATTGACACAC TACAAACATT ATAGAACCTG 300  
CAAAAAAA 308

20

(2) INFORMATION FOR SEQ ID :1009:

(i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 187 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :1009:

GAACCGCCTC TGTTTCCAGA GCAACTGGTC AAAACCTCTC CAAATACCGA 50  
35 GCAGTTTTGA AACTGGATT AGGAACCACT AATGAAAAAG AACAGACTCA 100  
GGGACAAGTG TTTGGCGGGA ATGTGTGAAG AGGTAATAA TGAGTCTCAC 150  
TGAATCACAC TATTACACAG ATGAAACAAA GCCTTTA 187

40

(2) INFORMATION FOR SEQ ID :1010:

512

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 175 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

5 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1010:

10

AAGAAAAAGA TATTAAGATG GGCAAGTCCT GGTGGCAAGA CAAGCAGATG 50

ACATTACAGA CAATGGACAT CAAACTGCTG CCAAGCTAAT TTAGATTGTA 100

15 AAAACAGCTC CATAGTCAAT ACCCATGAGT GATCTTAAAT ACGCACAATT 150

AAGCTACTTC TCCTTGATAT TACCT 175

## (2) INFORMATION FOR SEQ ID :1011:

20

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 208 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

25 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1011:

30

TGAAAAATAT TTGGAActCT TTAGTACAGA ACAGTTTCAA TATGAGTTAA 50

GAATCATGCG ATGACTACCA AAAAGCTAAT GCGATCCCAG GCTGCGGTAA 100

35 CAGAAGCAGA GCAGCTCAGC TGGGGAACGT GATAGTGATA ACTACTTCGT 150

ACTAGGTTAG ACTGTACCGA GAGACCTATG TTCAGTTCTG GGAGTGAAAG 200

TATTTTAT 208

40

## (2) INFORMATION FOR SEQ ID :1012:

513

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 184 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1012:

10

ATGATATCTA GACTACCAGT ATTTTTTGAA TGAGGCTTTC TTAGGAGTAT 50  
GTTGATGCAC TCTCATCCTT TCCTCCCCGG ACTCCTACCA CAACCCTCTG 100  
ACTGTGGAAT AGCATGGTTG TGTGTAAGGC TGGAGCACAG GCACAGTGAG 150  
ATGAGGATGA GGGATTGAGG GATGCTATAA GCCA 184

## (2) INFORMATION FOR SEQ ID :1013:

20

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 263 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1013:

30

CTTTGACATT TGATCAGACC AAACAGTGCT GTTCCCGGG GAGGAAACAC 50  
ATTTTAATAA ACACATCATC CCGCAGGCTC CCACCTTTAC CTCATGTTTC 100  
ATACCTTGTT TATCAAATGA GCGACTCAA ATGATTAAAA ATAATGCTGT 150  
TCTTTAGTAG CAACTAAAAT GTGTCTTACC GTCATTTATA TCTTTGTCAC 200  
CGGAAAGAAG CATTTTTGAT ACTTTACTGC GAGTCAAAA TCAATACGCA 250  
GAATGGCATT TGA 263

40

514

## (2) INFORMATION FOR SEQ ID :1014:

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 229 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1014:

CAAATTAAGT GCCAGAATGA TGCAGCCCGC TCTCACCAGG AAGAACGACA 50  
15 TGTGAGAAAA CTTATAGCAG ATGCAAAAAT GTCAACCCAC CATGTTATTT 100  
AAAAAAAAAT ATGACCAGGA TACAAGGACA CTTACCGTT TTTAACCCAC 150  
ACAAGGTCAG GTAATGTTTA CCTTGAAACA CAATCGCATA TGACCCTTTA 200  
20 TGCCACTCAC CTAGGCCTTT AATAATGAG 229

## (2) INFORMATION FOR SEQ ID :1015:

## 25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 246 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
30 (D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1015:

35 GAAAATAATG ATTCATATTA CCGGGTATTT CTTATCCAGT CTTTCATTCT 50  
ATGTAAATTG TGTGTGTGTC TATATATGCG TGCATGTCTC TCTCTACATG 100  
TATATGTGCA TATGTATGTA TATATATGCA TATGCACATA CATGCCACAC 150  
40 ATGCACATAT ACACACACTC ATAGAGAACA AAATTATTCC GAATATTTCA 200

515

TGAGGTTTCT TATTATAAGG AGACAATATT GATGCAATCT AATTAA

246

## (2) INFORMATION FOR SEQ ID :1016:

5

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 287 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1016:

15

TTCATAATCG CTGGCACTGA ACAAAGTTGC AGAATTCTTT GCCAGGTACT

50

TTAGGAAATC GTGAAGATAA TTGACTAATA AAGCAAGGCT CTTCTCATCC

100

AGAGGTGTAT AAGCCAACAT CGCTCCAATT CGTACAAATA ATCTCAGGAG

150

20

ATGTGGCGCT CCATACACCT GGGACATGGG TGCATCGGGA TGATCTGCAA

200

GAATTTTCAGC ATACTGTGGT CTCTCAAATT TATAGAGTAG CTGGGTACCC

250

25

AACATTACGT TGAAGTATTC TTTTATACTC GCCACAA

287

## (2) INFORMATION FOR SEQ ID :1017:

30

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 299 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

35

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1017:

ATATGAGAAA GCAGAGCAAA ACAGATGATG CTCTAAATGC AACTGACACA

50

40

CTTGCTAAAG ACGTTAGGTG CTCCATAAAT GCTTGTTGAA ATGCTGTTTG

100

516

TCAACATTG TTGTGAAAAA TTCATCTCTC CATCTAAGAA TCCTCATGAG 150  
TTAACCACAA TCAGTTCTAC ATAATTTAAC AGAAAACATC TGGTGGCACT 200  
5 TTTAAATGTT TAAGGACAGC ATTTACAAA CTAAGCCCGC CCCCAGTCCC 250  
ACTGCAGCAG GAGAAAATAA GGCTATGGAG AAAAGCAAGA TGAGTTATA 299

## (2) INFORMATION FOR SEQ ID :1018:

10

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 274 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
15 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1018:

20

ATTACTCCTT CTCTCGAATG CTTCCAGAAG AGTAGCACTC ACCACCTCAT 50  
GAGGAAAGGC ACTGCAACTT TGGTCAATGA TATCTGTTAG AAAGATCTTT 100  
25 TCCTATATTT AGAAGAGTGA TTCTCATACC TGAGCATGTA TGAGAATCAG 150  
TGGGTTTGAG GTGGGCCCAA GAATTTCCCT TTTTAACAAG TTCCCAGAAG 200  
ATGCTGATGT GGCAGCTTCT AGCACAGTGC TTGAAAATCC ATGAGTTTTC 250  
30 AAGAGGACAA TCTAAAGTGC TCCC 274

## (2) INFORMATION FOR SEQ ID :1019:

35

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 232 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
40 (D) TOPOLOGY: linear

517

(xi) SEQUENCE DESCRIPTION: SEQ ID :1019:

TTTCTTTGTC CTTGACAAAT ATTTATGGAA TGCCGGAAAT TATGGAAAAA 50  
5 CAATTCCAAT GTTACGAAGT CCAAAGAACT GGAATGAGAA AACTCCTCAC 100  
GGCACATTAT GCTGCATGGA ATGACAATCA TCCTCGGGGA ATTAGGGCAG 150  
CATCTTCTAC CACTTTTAAA GGCTACCACG AGACGGGGTG GAAATGCCAA 200  
10 AAATGGCACC TCATCTTTGA TCAAAGATTC AG 232

(2) INFORMATION FOR SEQ ID :1020:

15 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 133 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :1020:

25 AACAGTCCAT GCTGATCTTA GTAACATGA TGAAGATGGT GCTTGGCCTG 50  
TTCTTCTTGA TGAATTTGTT GAGTGGCAAA AAGTCCGTCA GACATCATAG 100  
CAAGAACTAT GTGAAGAAAA TGCAAACCTT TAC 133

30

(2) INFORMATION FOR SEQ ID :1021:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 280 base pairs  
35 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :1021:

518

	TCCTAGAACT CTGCTTGGAC CAGAAGATGT GAATAAACTT AAGCTTATTT	0
	ATTTAAAATC ACAAATGAGT TGCTCTAGAT TCTAAAAGGG TGAAACTTTG	100
5	ACTGTTGAAA GTTTAAGTAT TAGTAACTT GAGTTACTTT TTCTTTCAAA	150
	TTTCACTCCG CTCCTGCA TTTCGAAGCT GCTCTTTCTG GTCCTACCCA	200
	CCACCCCACC AACAAGACTT GTGTTTGTTA ATAGAAATAA TTTATCAAGG	250
10	TATTGGGGAT CCATTGTCTA TATTTAAAAC	280

(2) INFORMATION FOR SEQ ID :1022:

15	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 304 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :1022:

25	AAAATAAATA ACTTCTTAGA TTTTGGACTG AAAAGATCTG AGAATGTTCT	50
	GCCAAACAGC CGACCAACTG GTGCAAAGG TTAAGGCTGA CTGACTTAG	100
	CAACCTGCAG CACAACCAA AACACTGATG CAGTTCAGAG CTCTTCAAAT	150
30	GCATACTTCA GTGTTACACA CACATCAATT AAATTAGGTT AAATTAGTTA	200
	ATCCTCTAGA CAGTTTTCTT TTTGTTTTGC ATGCATCCCG TTCCATTTTC	250
35	ATTACGGGCA TCTATTCCTT GATCAATTAT GTGCTTTGCT TTTAATCGG	300
	TTTT	304

(2) INFORMATION FOR SEQ ID :1023:

40

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 237 base pairs

519

- (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :1023:

TTTCTTTGTC	CTTGACAAAT	ATTTATGGAA	TGCCGGAAAT	TATGGAAAAA	50
CAATTCCAAT	GTTACGAAGT	CCAAAGAACT	GGAATGAGAA	AACTCCTCAC	100
GGCACATTAT	GCTGCATGGA	ATGACAATCA	TCCTCGGGGA	ATTAGGGCAG	150
CATCTTCTAC	CACTTTTAAA	GGCTACCACG	AGACGGGGTG	GAAATGCCAA	200
AAATGGCACC	TCATCTCTGA	TCAAAGATTC	AGAGCAT		237

(2) INFORMATION FOR SEQ ID :1024:

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 320 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :1024:

30

GGCATGATTA	TTAGAAACTA	TTTAAGCTTT	TTTCTTTGAA	AAACAAGCTC	50
CTTTTACAGA	ATATAAACAA	CAGTAGTGCC	TGTGGTTTAG	CCCACCAATC	100
TTGATGACTA	AAAGTAGCTG	ATGCATTGTG	CATATGATGC	TTGAGATGGT	150
TTTTGCAAAA	GCAGAAATCG	CTGCAAGGTA	ATCACAATAG	ATAAAAGTGG	200
TATTTTAAAC	CTTTGAAATA	AATGGATGTA	ACTGTACCTT	GGTACAGCTT	250
TTCACTTGTT	TAGTTTTTAA	ACGTTAGTAT	AAGATTAGGT	AATTGAGGGT	300

40

520

TAGAGCCAAC AGGAATCTGC

320

## (2) INFORMATION FOR SEQ ID :1025:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 202 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
10 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1025:

15 TTCTGGCACC ACATTCAATA CTGATTCACA GGGATCTAAA ACATTCTAGT 50  
TATTCAGTCA CTCTGTCCTG TGTGGCAGAT AGGACTTATG TATCTTCAGA 100  
ATATTTGAGG AGTCATTCTC AGAGTCTCTC ATGAGTGCTC AACTTAACTG 150  
20 TTCCACAAGT CTGTCTTCAT AGCTGCATGT TGCATCTTCC AGTCTCTGTT 200  
CT 202

## 25 (2) INFORMATION FOR SEQ ID :1026:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 243 base pairs  
(B) TYPE: nucleic acid  
30 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## 35 (xi) SEQUENCE DESCRIPTION: SEQ ID :1026:

ATTGGTAGAC AATATCATAA GAGTTTTCTG ATAAAAGATG CTTTTTAACC 50  
CTGACTCCCA GTCACAATTT TGGCATCTCA TCCATGGGAA AAAAATAGGA 100  
40 AACTTATACA TTTCATAAAC TAAAGGTCAT CCAAACACTG CCAAAAACGT 150

521

TTTTATAAAT TGAGACCTAC TTACATCACA TCGGTTTTCC AAAGAGAATA 200

CACAGCGAAA GATGAGGCTC CACCCGGCCG GCACAGTCAT GAA 243

5 (2) INFORMATION FOR SEQ ID :1027:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 185 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :1027:

TATTTGCATT GAGGAAATAT TAATTTTCCA ATGCACAGTT GCCACATTTA 50

20 GTCCTGACTG TAGGAAACAC TGATTTTGTA AAGTTGCCTT TATTTGCTGT 100

TAACTGTTAA CTATGACAGA TATATTTAAG CCTTATAAAC CAATCTTAAA 150

CATAATAAAT CACACATTCA GTTTTAAAAA AAAAA 185

25 (2) INFORMATION FOR SEQ ID :1028:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 312 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :1028:

GCTTCTCTAT TCCTCCTGCC CGGGAGGAGT AGAGGAATTC TGGAGCCACC 50

40 TTAGTGGGCA ATGGGGGAGC TCCTGATGGT TCAGGAGCAG GAAATTTATG 100

AGCAGAGTGG GGTCCCAGGC CACAGGGAGA TGTCTATCCA CAAGGGATGG 150

522

TGGCCAAGGG TTGAATGGAA AGAGGCAGGC AGGGGGAGAG GGGCAGAGGG 200  
TGTGGGTATT CCCAGGGCCT TGAGAGTGGA CATGGCCCCT TCTCCTCAGC 250  
5 CTTCCATTAG CAAGGATGTC ACTGCTGCTC TTGCCTGATG ACAGCCAGAT 300  
CTGTTACAG TT 312

## (2) INFORMATION FOR SEQ ID :1029:

10

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 218 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 15 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1029:

20

ATTATTTATA AATTTTAGTG AGCACCACCA AAGTTAGGAT TCAATTGAGT 50  
TTGAATTCAA ATTCATTCAA AAGTTGCACA AATTTATTTT TTTTTCCTG 100  
25 AACATTCCTT TACTTCAGAT TGACAATTCA TTCTATTTAG AGCGCTATTT 150  
TAAGAAACCT TGATGAATCG CCCTTGACTA AAGGAAACAA AGTAGAATTT 200  
TATACAGATG GAAAAAGA 218

30

## (2) INFORMATION FOR SEQ ID :1030:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 base pairs
- 35 (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1030:

523

TTATTAGGGG GTTTAGAAAA TAAATTCGTA GGGTTTAAAC ATTGAATAAA 50

ACTACAAAAA AAGACACACA TTCAGGTAGC GAGGCTCTGG GGGTAACTCT 100

5 TTCTTAGTTC TTTGGACACA TCCG 124

(2) INFORMATION FOR SEQ ID :1031:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 237 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :1031:

TTTTGCCAAG TATATGTAGT GCAAATATTT TCTTTCAGTC TGTAGCTTGC 50

20

CTTTTTATTT NTAATGGGT ATCTTTAAAA AAATGGAAGT TTAAAGTTTG 100

AATGGAATTC AGTTTGTTTT TAAAGCTTGT GCTTTTTGTG TTCAACTAAG 150

25

GGATATTAGC TTACCATTTT TCTCGTTGA ATATTATGTG TTTATAGACA 200

AGAAATGGTC ACTAAAGCAA AATAACTGAA AATTATC 237

(2) INFORMATION FOR SEQ ID :1032:

30

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 147 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :1032:

40

ACAGCAACCG GCACTCACTT GGAATCCCAG TGTTCCGAGT TCTAAGGCCA 50

524

CTGAAAACCA TCAAGCGCTT GCCAAGCTCA AGGCCATCTT CGACTGCGCA 100  
GCGACTTCCT TGAAGACTGT TTTTAACATA CCAAAGGAGG ACAAGCT 147

5 (2) INFORMATION FOR SEQ ID :1033:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 238 base pairs  
(B) TYPE: nucleic acid  
10 (C) STRANDEDNESS: double.  
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :1033:

AGGCCTGCCT ACCGTAGGTC TCTCAGAGCC TTTACTCTAG TCACTCTTTA 50  
GAGGGGGGCA CTAGAAGCAA TATCTCCGAA ACTTCTTCGA CTGTGAGAC 100  
20 TTTTACTCA TAATTCGCTT CAAGCCAACT ACGGAGGCGC ATTTACAAAA 150  
CTGAAATACG AGCGACACCC CAGGAACGCA CGGAGACATG ACGCCCTTAA 200  
25 TCCTCTGTCC CTACTCCCTC TCCTAGGACA CCGCATTA 238

(2) INFORMATION FOR SEQ ID :1034:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 63 base pairs  
30 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :1034:

TCCATGNCTC NTGGTCTCTG TGCNCTTGNC AGGGGCATGC CAGGGCCCTT 50  
40 GGACTGTGCA GGG 63

525

## (2) INFORMATION FOR SEQ ID :1035:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 180 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1035:

CGACCGGCGC TCAATGGCGA AATTCCGAGC CAGAGCTATT GGTGAATGA 50  
GTAGCGCTGA TGGTTTAGAT AATAACTAGT ATGGGGATAA GGGTGAGCAG 100  
GCGCGCCTTG AGGCAAGAAG CGGGTTAGAG CATCTCTACT TAAAAGCCA 150  
AAGCCTATAA CGGTAGCGTC TACATCACGA 180

20

## (2) INFORMATION FOR SEQ ID :1036:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 142 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1036:

CCAAATACGA TGACATCAAG GAGTCGATCC GTCAGCGTGA CTTGAATACA 50  
CCACCGCCGA CGACCCGAAA GCCTGATGAG GAGAAGTCCA GAATCAGGAA 100  
CAACGGCGAC ACTCGACTAA CCATTTTAAA CCAATTGGAA CC 142

35

## (2) INFORMATION FOR SEQ ID :1037:

40

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 base pairs

526

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :1037:

CCACATGGAG TGACCTGGGC CTCTGCAAGA AGCGCCCGAA GCCTGGAGGC 50  
10 TGATTGTCAA AGCAGGGGGC AGGACCCGGG GGCAGGAGAA ACCAG 95

(2) INFORMATION FOR SEQ ID :1038:

- 15 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 195 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :1038:

25 ATTTTATTGT AGTAAGAATA ATACATAGAA ATAACATTAA ATAAATATGT 50  
TTGACAAAAA CATAACACA TAGTACAGGT AGAACATATA ACTGGTTGAT 100  
GCTAAATAAC AGATCCAGAT AATTTTCAAT TTGAATTAGC AGCAGGGAGT 150  
30 CATTGAATGC TATGCCCTTA GAATGGCTTG CAGGCTTTCA CGAGT 195

(2) INFORMATION FOR SEQ ID :1039:

- 35 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 218 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

527

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1039:

CGTTGTCAAG AAAATGAAAG GTAAAGCTCA GAAGGGATAA GGGAAGACAT 50  
5 TACAGAATTT ATCATCAAGC AGGAGGTTTT TTCCAGGTTC TAAGATGAGG 100  
TTAAGTTTCT TAACAAAAGA ATAAACAACT GTGACTCTAT CTGTCGGGGG 150  
AGGGTCTAGA CAGAAAAAAT GAATATACCC CAAAAGGCTG AAAAAAAAAA 200  
10 CGAGACTTTG ATGGAGAC 218

## (2) INFORMATION FOR SEQ ID :1040:

15 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 318 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear  
20

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1040:

25 TTTATTATTT TGAATGATTT AATGGTTTTT TACACAATTT ACATCACAAC 50  
ATGTAAATTT TAGCAGTAAC ATCTGATTCT AACAGCACAT CATGCTATTC 100  
CTTTCATAGA GCCTTCAGAG ATTCAATGCT AAACAAATTT CCTTAGTTGG 150  
30 CATCAAGGCA CTGATCACTT TAGAGGCTTT TAAGAAATTA TTAAAGATG 200  
CAAATGCCTC TGAGTGAAGT GTACTATCCC ATCACTGAAG CCCACAGGAA 250  
35 CAAGTCCTAC AATTTTAAAA AGGCTCGATG GAAAAATTC TCAATCCTGA 300  
AATCCCCTAG GGAAGGGG 318

## (2) INFORMATION FOR SEQ ID :1041:

40 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 199 base pairs

528

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1041:

ACGTACCGAG	CCGTCGTCGC	GGTGCTTGAG	CTTGAAGGCG	AGATAGCCGA	50
TGCCGCCGAG	GCGGTGGACC	GCATCACGGT	GGCGCTGACG	AACGCGAGAT	100
TCAGCAGCAG	CGATGCCATC	AATAGCAGCC	TGATCGGACG	CATGACCGAC	150
TCTCCCTGTG	AGCGGAGGTT	GGGGGGCCGA	TCTCCCGCCG	GTGCCGGGC	199

## (2) INFORMATION FOR SEQ ID :1042:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 300 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1042:

GCCTCTAACA	AACTAGGCT	GTCCCGGACC	ATGGTAATAG	AATTGTTTAC	50
CTTTATACCA	AGAAGGTTGG	GAAAGCACCA	AAATCTGCAT	GTGGTGTGTG	100
CCCAGGCAGA	CTTCGAGGGG	TTCGTGCTGT	AAGACCTAAA	GTTCTTATAG	150
ATTGTCCAAA	ACAAAGAAAC	ATGTCAGCAG	GGCCTATGGT	GGTTCCATGT	200
GTGCTAAATG	TGTTCTGTAC	AGGATCAAGC	GTGCTTTCCT	TATCGAGGAG	250
CAGAAAATTC	GTTGTGAAAG	TGTTGAAGGC	ACAAGGCACA	ATGTCTGGAA	300

40

## (2) INFORMATION FOR SEQ ID :1043:

529

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1043:

10

GAGACCAGTC TCAAGTGGGA GGGGCTGATG GTGGGAAGCC CTAGAAGAGA 50  
GTCTGGGATG AAGCGGCCTC CTCCCTGTCT TGCCCTCCAA AATTGAGTCT 100  
GGCCTGATTC CTTTGAGGAG CAAATTTTAC AATCATCCCT CACCCTAACA 150  
CACGGTGAAA CTGGAAAACC 170

15

## (2) INFORMATION FOR SEQ ID :1044:

20

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 260 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1044:

30

GGCCCCCCT GGGGACTGCT GGTTCAGG GGCCACCCC CCTCATCCAA 50  
AAGAAGAATC AAGTTTTGTT TTCCTGTGGT TCCCTTGCTC TCCCCGGCCT 100  
CACCTCGAGC TTCCACTTGG GCCCTTTCCC ATGCTTCTAC TTGAGCCCCG 150  
CCTGCCTCAC CGTCTGCCTC ACCGCCACCT CCTGCTCAGA GTGAGTGCAT 200  
GCATGCCAGA CAGATACACA TATACATACA CACACACACA CACACCCTAT 250  
TTTTTTTTTTT 260

40

530

## (2) INFORMATION FOR SEQ ID :1045:

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 164 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1045:

AAATCTATAA TTTTAAGGGC TTAACCTGTG ACTTTAATAA GCTGGAACAG 50  
15 TCCACTGAAT GGGTATAATG AATTGCAGTA TATACGTATG ATCGCTTTTT 100  
AAGTGATTAT CTTTCTTTC GTTAAGTCAT GTAAATTCAT AAATTTTTTG 150  
GCACTGATGT GTTG 164

20

## (2) INFORMATION FOR SEQ ID :1046:

## (i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 130 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1046:

TCCCTCCTTT CCGAACTGGA GCCCCATCCT CTCCAGAGTA TCCAGGGCTT 50  
35 CTTCACTCCC GGGTACCTGC CCTTCGGCCC CTTTTCACCA CAGCTGTGCT 100  
ACTGTCAACC AGTCTTTGCT GCATAGGCAT 130

40

## (2) INFORMATION FOR SEQ ID :1047:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 285 base pairs

531

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :1047:

10 GCTTAACTGG AAATTGGAAG GGAAAAGAAG AAGAAACAAT GTAATGTAGC 50  
AGTGGAAGCA AAATTCTCAC AATGAATAGC AGTCTTTCCA GCTTCTTTGA 100  
CACGGATTTT CTCATTAGAA AAGACGACTC TCCTGAACTA GGGATGAGTG 150  
15 TGAATCTCCA TTCGAGGAAG GGGAAGAAGA GCTCGGAGGG TGACAGCCTC 200  
CCCCTGAGAG AGCCAGTTGC GTTCATGATT TTGATTCCTT CTCCTCCTG 250  
ATGAAGTATC TGCCCAGGAG CCCAGGAGCA GAATA 285

20

(2) INFORMATION FOR SEQ ID :1048:

(i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 233 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :1048:

TAAAACTGAC CTAGAAGCTA TCAGCAACCA CAAAGAGACA GAAGAAAAGA 50  
35 CTGCTTCTGA GGCTCTCTCA TGGAACCTAC TGATGATGGT AATACCACGC 100  
CCAGAAATAA CGGAGTCGAT GATGATGGCA ATGATGACGG CGATGATGAC 150  
GGCACTGATG ACCCCAGGCA CAGCGCGAGT GATGACTACT CAACACGAGC 200  
40 CAGGTCTTTC TGAAGGCCGA GAGAGCTAAA TAA 233

532

## (2) INFORMATION FOR SEQ ID :1049:

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 293 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1049:

ACTTTAATTT ATTTCGGATG CCGGAATTGT GCCCAGAGTT TCTCCTGAGC 50  
15 TTGATTCCAT AGCTAGCAGC TTCAATCCTT CGCAGCTGCG GTGCGTTCTG 100  
AACTCTGAGC TGTCTTTTCC TGACAGGCAC TTTCCATAGC ATCTGCCTGC 150  
TTAATTCCTC ACGACTCAGA AATGTTAACG GCACTGTCGA GTGCTGTGAT 200  
20 CATTTTGCTT TAACTATGTA AAGCTTTATG CCCTTCGAGA AGCTTATTTC 250  
GAGATAGAGC TAGAGAAGAA AAGCAGCAAA ATTCGGTCGA TAC 293

25

## (2) INFORMATION FOR SEQ ID :1050:

## (i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 219 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1050:

AAAACTATAC TTTCATTCAA AAGAAGAGCT GAATTGATGC TTGAGTTACA 50  
GCACAAATCT ATTATTAGTG AATGAAGTAT ATTCTTGCA GATAAATACC 100  
40 AGATCAAAAG TCCTGTTTCA GTAATTTGAT TAACTGTAG AATACTAAAA 150

533

AATAAGTTAT TTCTACAGAA ATCTTTGAAG GGAGCAAAAA ATCAAATCAC 200  
AGTATATACC TAATGGCTA 219

5 (2) INFORMATION FOR SEQ ID :1051:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 70 base pairs  
(B) TYPE: nucleic acid  
10 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :1051:

AGCGACCGGC GCTCAAGTGG AATTCCGTGC AGTGTTTGAT TTTTCGTTTT 50  
TGCGATAGTT TACTGAGAAC 70

20

(2) INFORMATION FOR SEQ ID :1052:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 204 base pairs  
25 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :1052:

ATTCCTGACC TGTGATATCG GCCATTAGAG CCTTTCAAGA ATGGTACCTC 50  
35 CTGCCGATGA TTTTTTTTAA AGCCTTAATG AAGAGAGTGT CCTCTGACTC 100  
CTTCCAGAGA AGATAGGATG TGACTGAGTA AGTTATGTAT AATAATTTTA 150  
TCTCAAATA ACCACGTCCT TGATACCATT CCCTGTATAC CAAGGAAGGG 200  
40 TATT 204

534

## (2) INFORMATION FOR SEQ ID :1053:

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 252 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1053:

ACTAACACA GCACTGAGAA TTCTCCTCTT TTTACAAAAA TGACAGACTT 50  
15 AAGAGAGGGC ATGGAACAGA TTAAGAGAAT TAACACGGAG AGGAGAGCAG 100  
AGGTATAAAA GGTATCCAAG AAAAGTAAAA CATACAAAGG CAATTCAAAT 150  
CAAAGTGAGC ACTGCCTATA TACAGACAGA AAGCGAGTCC TCTATGAAAC 200  
20 CATACCCGAC AGAAAGTACC GGAATACCAC CGACACTGAT GTCTTCCAAA 250  
CG 252

## 25 (2) INFORMATION FOR SEQ ID :1054:

## (i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 212 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1054:

AAATCAGGAA ATTGTACATG TTAACAAAAT AGTATAACCA TGCATACATA 50  
CATCTGCTTA TTAACACTG AAGTAAAAGA ACTAATCCAG TTTGCAGTCT 100  
40 TTAGAGGTGT TTAGTATTTT ACTCCGTTCT GATGGAAGCA CTTTGAATGC 150

535

TTGCATGGAG ACATAAACT GAATATTTAA TTGACAATAG ATCATGCGCC 200  
TGTATTTATA AA 212

5 (2) INFORMATION FOR SEQ ID :1055:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 152 base pairs  
(B) TYPE: nucleic acid  
10 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :1055:

ATAAACTGTG CTAATAAG TTTTATTTT ATCAATATAA AAGCTGTAAA 50  
AAAACCTGAGG AGAAAGCAGT TGCCAAAAAG ATGAAAGAAA AACACATAG 100  
20 AAAACCTTTA AAACAGGCAA AAGTCAGTTC ATAATAAAGT AACTCATCTC 150  
AC 152

25 (2) INFORMATION FOR SEQ ID :1056:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 205 base pairs  
(B) TYPE: nucleic acid  
30 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :1056:

AACAGATCCT CAGTTTCTCT GGAGACACCC CCAATTCTCG GGTGAGTGTT 50  
GAAACCTGAC AACTGACTGT TAGCCTTGTC ATCATCCTCA TTGGAGATGG 100  
40 AGATGTTGTA GTCGGAGCCT CATTCCTTCC GGGGCACTGT TTCTTCTAAT 150

536

GGCAACCATC AGAGCCTGTC TGGAAACAGC CTGCTGCCTT TGCTAGGGGG 200  
GCAAA 205

5 (2) INFORMATION FOR SEQ ID :1057:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 174 base pairs  
(B) TYPE: nucleic acid  
10 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :1057:

GAGAGAAGAG CGCTTTTCTG GGCTCTTGGT TACTCCGTCA GAGACTTTGC 50  
CCTTTGTCTG TTAAATACA CTGGGAGCCA GAGCTGATTC CCCACCTGCT 100  
20 GCTGTGGTTT TCCGCTTAAC ACAGGAGAGA TGAGTTGGTC TGGTATATTT 150  
GATAGCAGGT TTAAAATGA ATCC 174

25 (2) INFORMATION FOR SEQ ID :1058:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 125 base pairs  
(B) TYPE: nucleic acid  
30 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :1058:

TATTTGATGG TCCATAAGAC TTTGTCAAAT GTAAACCTAC AGTTTGATAA 50  
GCTTTAAAT ACCATGTTGA CAGCATTTTG AATTGTTTCA TAGACGTACT 100  
40 TATTAACTG ATGCGAACAT TCACA 125

537

## (2) INFORMATION FOR SEQ ID :1059:

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 205 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1059:

TTATCTTACA ATTCTACTTC CCAGCATCCT GAAATTTTCA AATACTGTCT 50  
15 TAGTATATTA AACTCTTTTG AAATAGATAA CAAAAGCACC ATGGGAGTCC 100  
GTTGAAAAC TTAGGTTTGTT CCTTCTAAAA TTTCTAAGTC CTCATTATG 150  
ACTATAAAGA AAAAAGGTTC ATCAATTCAA AAAAAAATCC TGATTCTTCA 200  
20 AAATA 205

## (2) INFORMATION FOR SEQ ID :1060:

25

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 249 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1060:

35 ATCTCACAGA TTCTTTTTC AAGATTCATT CATGTTGAGT GAAAGAAGCC 50  
AGATGCAAGA GTCCACACCA CATGATTCTG TTTCTATACA ACTTAATTTG 100  
AAAAC TAAGC AATACTTACA GAAGTGAGAA TAGTAGTTGT CTCAGGGTAG 150  
40 GTGAGTGTC TGAAGGGAAT CTTATACGTT TGCTAAAAAT GTTTTATAAT 200

538

ACTTGGATTT TGGGTCTA 3CTGGCAGG GGAAGGATA CATTGCAAA 249

(2) INFORMATION FOR SEQ ID :1061:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 200 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :1061:

15 TAGCACATTG CATCCAAGA GCTGTAGTCA AAATCCTCAA AATCTGATGA 50  
AAATGGCATA CTACACTAAG GAGGATTTTT TGGGCATTTT CCATTCATAT 100  
GCAGAATCAG TGGTTGAAAA AGGAGAAAGA GAGATTTTCT TTACAAAAGC 150  
20 TCCTGACCCC ATTAACATCT TATCTATAAA TCTGATATGT TCCTGACTCC 200

(2) INFORMATION FOR SEQ ID :1062:

- 25 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 200 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :1062:

35 GCGCACAGCT GAGAATCTCC GGTCTTGTCT CACTTTGGAC TGGGACAGTG 50  
GATGCCCATC TAAAAGTTAA GTGTCATTC TTTTAGATG TTTTACCTTT 100  
ACAGCCATAG CTTGATTGCT CAGAGAAATA TGCAGAAGGC AGGATCAAAG 150  
40 ACACACAGGA GTCCTTTCTT TTGAAATGGC CACGTGCCAT TGTCTTTCCT 200

539

## (2) INFORMATION FOR SEQ ID :1063:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 246 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1063:

TATCAAATCA TGAGTTGAAA GATTTTGACT ATTGAAAACC AAATTCTAGA 50  
ACTTACTATC AGTATTCTTA TTTTCAAAGG AAATAATTTT CTAAATATTT 100  
GATTTTCAGA ATCAGTTTTT TAATAGTAAA GTTAACATAC CATATAGATT 150  
TTTTTTTACT TTTATATTCT ACTCTGAAGT TATTTTATGC TTTTCTTATC 200  
AAATTCAAAT CTCAAATCA CAGCTCTGAA TCTTAGAGTA TCATAA 246

## (2) INFORMATION FOR SEQ ID :1064:

25

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1064:

CCCTCATGTG CCAGTTCGGT CTGCCTGCAG AGGCTGTGGA GGCCGCCAAC 50  
AAGGGCGAGT GGGAAGCGTT TGCAAAGCCA TGCAGAACAA CGCGCAAGTT 100  
TGAGCAGAAA GAGGGCGACA CGAAGGACAA GAAGGACGAA GAGGAGGACA 150  
TGGAGCCTGG ACTGAGCCAC 170

540

## (2) INFORMATION FOR SEQ ID :1065:

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 171 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1065:

CTCTCCCCCA CAGGTTCTCA GCAGTTACTA AGATGTCCCC TGATTTTCATT 50  
15 GACCTCTGTG TGTCTTCAGT CCTTGACCCT TTAAGGCTCC CTGGTGCCAG 100  
AATGTCTGCA GCTGTAGGAT CAAAGACCCT TGGGGGAAAA ATCCATTCTC 150  
AAAAGAGAGG AAGATGGGGT G 171

20

## (2) INFORMATION FOR SEQ ID :1066:

## (i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 201 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1066:

GAGTCTATAT CCCTTACTCA GTGCAGTTCT CAAAGTCCTT TGTATGTCGT 50  
35 ACAGGATCAC ATCTGTACAT ATCACACTCT TGTGGGGTAA GCCCAGAAGC 100  
TCATACACAG CTTTCATGGGT TTTACTTTCCC AAGCACTTCC TCCCTCCCTG 150  
CAATATCTCC CCAGCACTTT CTGCTTCCTA TCAGCTTTCC CCTTTTTCAA 200  
40 C 201

541

## (2) INFORMATION FOR SEQ ID :1067:

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 151 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1067:

ATCAACCGGA GGTGAAATGA AATACCGTCA ACCTGTGCAT GAGTTTGTGT 50  
15 GAACTGAATG TGTGTGCATA CACATAAGCA TGTGTGCGAG CGCAAATGTG 100  
GCGTCTCCAC AGCATGCGCA ATCCATGAGT CTGTTTCTAA CGCGCGCGCG 150  
C 151

20

## (2) INFORMATION FOR SEQ ID :1068:

## (i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 273 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1068:

ACTGTGTCAT GTCAGGTTAG ATCTGAATCT CTAGGAGAAT AGCTTTTTTG 50  
35 ATCTGTTTGC TCCTTTGAGT CTCCCTTTTA CTTTACAACT AGAAAACCAA 100  
TCGCATACTT CACTTCTATC GCTTCCAGAT ATGGCATATT TTTCTTAGGC 150  
TACCGTTGAA ATTTAGCATA ATATTTCTCC CTTACCTTTA CGTCCTTTTA 200  
40 AAAAAATAGG ACTATAGTAA GTCCTCCGTG TCGGTGGCAT GTTTTTGGAA 250

542

ACTGACTTTA AAGAAAACAT ACA

273

(2) INFORMATION FOR SEQ ID :1069:

5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 189 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :1069:

15

CAATCTTGCT TATAAATAA GAACACCTTT CAATTAAGTG AGTGGGTCAT

50

TCCTGGTGCA ATTGTGATTT TTTTITAGCC AAAATGAATG GCAAACCTCTA

100

TTTAGAGCAA AGTAAGTATT AGAAAACCCT AGGAACTCTT AATCAACGTT

150

20

TATTACACTT TTATAAAGGC AACTACGCG AAAGAGCCC

189

(2) INFORMATION FOR SEQ ID :1070:

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 280 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :1070:

35

TTTATTCCAC TGGAGAAAGG GGATTGAAAA TCAGTTAGAA CCAATGTATT

50

TCTTGCCCCA CGGAACACTA TTCCTATAAG ACAGCTGAAA GAAGCTGCCG

100

TGAGGAGCTC AGCTCCAAAC ACAGGATCAG CACCTCGCAT AGGAATTCCC

150

40

ATGAATCAG ACTTCTCATC CCGTTTTATC AGAGTGCATA TACGTCCTAC

200

543

TTAAGGAAAA GTAAAACAGT CATTTACGAA AGAAAGTCAA TCTGTATCCT 250

AAGCATTTTA ATAAAAAGTC AGAAGGAATT 280

5 (2) INFORMATION FOR SEQ ID :1071:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 193 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :1071:

AGAACCGAAG CCTGCAGAGA GGCCATTCTG ACAGGCTGGG AAATGTAGCC 50

TACCGCCAGA AGCTAGAAGC AAGCACTTCC TCCTAACCGA GTTTTTGAAA 100

20 GACTAAGGGA AAGAGAATAG AGAAGGGATA TTCCCATCTA CCGGGGAAAA 150

GATGCGCAGT AACAAACCAT CTAGGGAGAC AGCCTTCTAA CAG 193

25 (2) INFORMATION FOR SEQ ID :1072:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 175 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :1072:

AAAGCACCTT CCCCTCGCTG AGCTCCAGGG GGCCCAGATA GGCCACGCGC 50

AGCTCCAGCA TCTTGGAGAG CTGCACGTCA TCTGCCGCGT CGTAATCCTC 100

40 CACTCTGCAG CCATAGGCCC CACTCTGGCC CCGGGTCACT CCCTCCAGGG 150

544

TCAAGTTCCC CTCGAGATTC ACATC

175

(2) INFORMATION FOR SEQ ID :1073:

5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 339 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :1073:

15

AGTGCCCTAC TCTTTTCCCA AGAAGGGTCA AAGCCTACAA TATCATCAGG

50

GGGCATGAAG CACATTAATT TGCAGTGGCT GCTTCATATG AGGAGGTATG

100

GTGGACAGGC TAATTTTCC TTGAAAATGT GGCTTCTTCA ACTCCTTTCA

150

20

AATTTAGGAT GGAATACTTC CTGAAATAAA AACTGGGCTT TATGCAGGAT

200

TCTCTTTGAA AATTCTTGTA TGTCCAGAAC AAAAGATAAA ACTAATTGTA

250

25

TTCCTCACAT TCACAATCCC CATTGGTCTG AAGTCACGTG ACACAGAGCA

300

TCTATATAGC ACATAGTGTT TAAAGACTAA TGAATGCAA

339

(2) INFORMATION FOR SEQ ID :1074:

30

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 172 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

35

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :1074:

40

ATTAATTATG CGGTCCTCCT CCTGGCAGCT GGACACCAGT TTGAATCTTC

50

545

CTTTGAGCTC CGGAAAGTTG GTAATTACAA CTTGATATTT CTACATGGAA 100  
ATCAAGAAAC TCGGACCCAA CTTGGTGCAA AGACGGATCT CCGCCGATTC 150  
5 TGACGGCTCT CCAGGTTTTG TC 172

## (2) INFORMATION FOR SEQ ID :1075:

## (i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 299 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear
- 15

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1075:

AGAGTAGGAA GAGGGAGGGG AACAGGCATC TAAGATAGAC TTTCTCCATC 50  
20 TGTGTTGGAGC CTGGGCAAGT AGGAAAGAAG CCTTTTTCAT ACACTTCAGT 100  
CGTATGACTG AGCTGCTTGG CAGGGCACTG GAAACGACGA ACTCGCGCAG 150  
25 CCTGCAAATG AGACCACTCT CATTTCTCAG TTTCGATTG ATTCACTCAC 200  
TAGTAGTTAG GTAAATACGA GCTCTATGTG ACTCAAGGAA TGTCAGGCTG 250  
GGGCAGGTGG CAAAAGCTAC AGTGATCGAA ATTCACGTTG CTACTGATG 299

30

## (2) INFORMATION FOR SEQ ID :1076:

## (i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 283 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear
- 40

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1076:

546

	GCCCTCATCG GCGATACTGG AGGTTCGCTT TCTCAACCCT GTGGGCTTCA	50
	CCCCAGACAC GCCCTGAATC GTTTCATGTT CCAGCATGCC TGAGACAATC	100
5	ATCGACTGAA GGATGTTCTC TAACACCCGC ACGAGCTGCC GGCAGATCTG	150
	AATGCCCAAG TCACTCAGCA CCTGCCGATA CTCAGCCAGG TCAAAATCGG	200
	CGAGGTAGTG CTCATGCCTG GCGAGACGTG TTGTGCTTAA TGAAGCCCTA	250
10	TCATTCGAAG TATTGCTATG AGCAGTGCGA AAA	283

(2) INFORMATION FOR SEQ ID :1077:

15	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 297 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
20	(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :1077:

25	ACCAATCAAG TACTACTAAAT TAGAATATTT TTAAAGTATG TAACATTCCC	50
	AGTTTCAGCC ACAATTTAGC CAAGAATAAG ATAAAACTC GAATAAGAAG	100
	TAAGTAGCAT AAATCAGTAT TTAACCTAAA ATGACATATT AGAAACAGAA	150
30	GATATTACGT TATGCTCAGT AAATAATCAA GAGATGGCAT CGCGTAAGAA	200
	GGAGCCCTAG ACTGAAAGTC AAGACATCTG AATTTCAGGC TGGAAAACTA	250
35	TCAGTATGAT CTAAGCCTCA GTTCTCTNGT CTGCAAAATG AAAGCAC	297

(2) INFORMATION FOR SEQ ID :1078:

40	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 291 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double

547

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :1078:

AATCTTTTAA TCAATCGAAA CCTTAATAAT TAGGACTGAT AATAGTGATC 50  
AGTGATTGAA CCTTTATTAT TTACCAGCTA ATATAGTAGG CCCATAAATA 100  
10 GGTATATCA TTCGTAGTCA CAATAACCAC ATACATCACA CACCATGACG 150  
TAGCGCTACT ACCCATACCT GCTAGCAGTC AAGGTTTCAGA TAATCATAAC 200  
15 ACGCCCAACA TCTCATTGAT AGTGAGTTAT CCAAACAGGA ACAATCTCAA 250  
GTTTATATCT AAAGCCCATG TTCTTTTGCT TAATATTAGA G 291

20 (2) INFORMATION FOR SEQ ID :1079:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 136 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
25 (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID :1079:

AGTCACAGCC CCTATACTCC CTCTACACAT TAACCACAAC ATAAGCGGGG 50  
CTCACTCACC CACCACATTA ACACCACGAA ACGGGTAATC TAACACGAGA 100  
35 AAACACCCTA ACGTTCATAC ACCCCATACA CCATTA 136

(2) INFORMATION FOR SEQ ID :1080:

(i) SEQUENCE CHARACTERISTICS:  
40 (A) LENGTH: 300 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double

548

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :1080:

	CCAAGGTCGC CTGTGTGCTA GTCACGACCA TTAGGATCCG AAGAAGAGAT	50
	GATGACTACC CTAAAAGTAA GGTCTGTGAA CAGCCTGTAA TGGGACGTGA	100
10	GCTGCGGTAT TAAAAAATC AAGAATGGAA GCGTTCCTCA ATTGTCGTTG	150
	AGAATCATAC CAACACGGCA GATGCAACCA TGAAAAACGC AGCTGCGTAT	200
15	CGCGCGTTTT TCATGGTTTC CATCTGCCGT GTATGCAATG ATTCTCAACA	250
	CACATTGGAG TCACGCGGCC TGCCTAAGAG TATGAAGGTC TTCCTGTAAA	300

20 (2) INFORMATION FOR SEQ ID :1081:

	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 219 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
25	(D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID :1081:

	GTTAATGGTT TTTTCATACA TATGAGACTG AGCGGTCAA GTTTTACTAA	50
	AGTCTTTATG ATCTTTAATT AATACTCCAA GACATCCGAG TTTGGCAGAT	100
35	ATTGGATGAG ATTTGTTTTG CTCCTTACTT TCTTTGTATA CAGCCAAGCC	150
	TGAAAATCTC TAGACATTTG CTGAAATTGA TGAGAGCATG CACAGGACGA	200
	CTGAAGGTGC TGGACATGA	219

40

(2) INFORMATION FOR SEQ ID :1082:

549

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 360 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1082:

10

ATTTTGGGAA AGTGAGCATG AAGAAGGGAC TCAGAGCTGC CAGGTACCCG	50
AGTCTCAGGC TCTGACATCT CTTGGGGCCC CCTTCTGCCA CAACTTCTTG	100
CCACTTCACG GACTTGAATT ATGTCCCGCG CCTAAAAAAA AGATTGGCCT	150
GCAGCACAGG CGTGTATCCT CTCCAAAAAG CTGCTGCTCA TTTCTGGCCC	200
CATCTGCTGC TATCTTTGCC AGTCAGCCAT CACAGTTTGG CATCATCAGA	250
GTCTCAGCTA GAGGGAGCGT GTCATTTCTG CCTTAGTGGT TTGCCTGCGA	300
CCTGACCAGG GCAAGACCAG CTGGGATGTC AAGTGACATT TTGGGAACTT	350
GTCGGAAGTT	360

15

20

25

## (2) INFORMATION FOR SEQ ID :1083:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 250 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

35

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1083:

CATACATATG AGACTGAGCG GATCAAAGTT TTACTACAAG TCTTTATGAT	50
CTTTCAATTA AATACACTCC AAGACATCGA GTTTGGCAGA TATTGCGCCC	100

40

550

GCCGTTTTGC TCTTCTTATC TTTGTATCCA GCCAAGCCTG AAAAGTCTCT 150  
AGACATTTGC TTGAAATTTG ATGAGAGCTT GCACAGGCCG ACTGAAGGAT 200  
5 GCCGGACATG ATTCTCTGCT TTCTGGTTCA ACAAAAAAAAA AAAGTTCCAG 250

## (2) INFORMATION FOR SEQ ID :1084:

## (i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 261 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear
- 15

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1084:

TNCTAGATAC NTCCCTCTGT CTCACATTCA TAGTGTGTTT TTGTCTAGTG 50  
20 TATGAAGTCT CACNCAAGGA AAGTGTNCAG GCAGAGTTTG GGGAGAGTGA 100  
AAAAAGTGAA TGGCCTATAT NTGCTCTNTT GGGTGNTCCA NCCATTATTG 150  
25 GGGTGAACCC TTTCAGCTTT TTCCTAAAAA TTTGAAAAGA NTTTTTTAAA 200  
AAATTAAAAA GAGGATTTTT AAAAGGAATA TCTTGTTCAA AATTNTTAA 250  
GTTTTAATAG G 261

30

## (2) INFORMATION FOR SEQ ID :1085:

## (i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 260 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear
- 40

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1085:

551

GCAATCCATA AGTGTCCTTA TCTACAAAGT GAAAAGTTGG ACAAGATATT 50  
CTTCATGATC TTTTTCGATT TTAAAATGTC ATGCAATTTT AGAGAAAAGC 100  
5 TGAAGGGTCA CCCAATATGG CGCGACACCA AAAGACAAAT ACGAGGACAA 150  
TCACTTTTTC ACTTTCGCA AACTATGCCT GGACACTTCC TTGGCGAGAC 200  
TTAATACACC AGACAAGAAC AACTATGAA TGCGAGACAG AGGGAGACAG 250  
10 AGGCGAAATA 260

(2) INFORMATION FOR SEQ ID :1086:

15 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 213 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :1086:

25 AAGACGTGGA TTTGCTGGAA GACACGGATT TCCTGGAAGA CCTGGATTTT 50  
TCGGAAGCTA TGGATTTGAG GGAAGACAAG GATTTTCTGG AAGACATGGA 100  
TAATCTGGAA GACATGACTT TGTCGGAAGA CGTGGACTTG CCGGAAGACA 150  
30 CGAATTTCTT GGAAGACCCG GATTTTTCGG AAGCTATAGA TTTAAGGGAA 200  
GACAAGACGG ACT 213

35 (2) INFORMATION FOR SEQ ID :1087:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 256 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
40 (D) TOPOLOGY: linear

552

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1087:

5 TCCCAGGCAC CCGCTGAATT TCTGAGGCCT TGCTTAAAGC TCAGAAGTGG 50  
TTTAGGCATT TGGAAAATCT GGTTCACATC ATAAAGAACT TGATTGAAA 100  
TGTTTTCTAT AGAAACAAGT GCTAAGTGTA CCATATTATA CTCGACGTCG 150  
10 ATCATTCTC AGTCCTATTT CTCAGTTCTA TTATTGAGA ACCTAGTCAG 200  
TTCTTTAAGA TTATAACTGG TCCTACATCA AAATAATAGA AATTACGTTT 250  
TTTTTT 256

15

## (2) INFORMATION FOR SEQ ID :1088:

## (i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 264 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1088:

TTGCTTAGAA CGGAGCTAGC AAGACAAAAA TACTTCAGTT GGCATCTCCC 50  
30 TTAAAGCACA TCCCCAAACG CGGGTCCTGG CCCAGACAG GGAGACCAGG 100  
GCTCTGACAG TGACAGGTTT TTCCCTCTGA AAAAGAATA GAAGAGGAGC 150  
TCCTCCCTAA CCCACAGATT CCCAGGGCAG ACCCTGGGAG GAGGTGCTGA 200  
35 AACACAGAAG AGAGTGTGTC TTCCCCAACC TCTACCAGAC AGTAGAGAAA 250  
CTGAGGCGAG AGGC 264

40

## (2) INFORMATION FOR SEQ ID :1089:

## (i) SEQUENCE CHARACTERISTICS:

553

- (A) LENGTH: 157 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :1089:

10	GACCTGGAAT TTGTTTTCGT CTGTTTCAGTA GACTCCGATT TCAGAATATG	50
	TCGGAATTTC AGACTCCGGA ACTTTTGAGA ATGTCATTAC AGGAACTTTG	100
	TTTACATACC GAGCTGTTAG CCCAGTCAC TGGGTCCGAA ATTACGCCGA	150
15	TACCGAC	157

(2) INFORMATION FOR SEQ ID :1090:

- |    |                               |
|----|-------------------------------|
| 20 | (i) SEQUENCE CHARACTERISTICS: |
|    | (A) LENGTH: 366 base pairs    |
|    | (B) TYPE: nucleic acid        |
|    | (C) STRANDEDNESS: double      |
|    | (D) TOPOLOGY: linear          |

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :1090:

30	GCATATACCA AAAAAGGACA AACAGATAGA AGAGTCATCT CAGTGTGTAA	50
	CGAGGAAAAG ATTTATCTCC CATCCTCTGA TCCTCCATAT GATATCTGAT	100
	AGCGAAGATG ACAATAACCC CTTGACTCTT CACGAAACT CGATGAGAGA	150
35	GAACTTGAA AAGTCAGAAA ATAAGTTCAT ACCGCAATTA ACCTTTTGGT	200
	CAAGTAATGG AAACCTTTTGA CTACTAGTGT AAGTCAAAAG ACAAAGGACT	250
40	CCAGCAAGAT GAGAGATTTT TCTATTTTGT AACGAGTAGT CCACCGATCG	300
	TCATCAAAGA GAGAGAATGA ACAACTACGA AAGTTTAAGG GAAAAAAAAA	350

554

AAAAAACATA GATGTT

366

(2) INFORMATION FOR SEQ ID :1091:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 305 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
10 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :1091:

15 GGTCTGAATC ATGAAAAGC CCATAAGAGA GATACAGTGA CTCCAGTTTC 50  
AATCATATTA CAGGAGATGA ATCTGTTGCT CTCCCATTTT GCTCTTGTC A 100  
CACCATATGA AGACATCAAA AAACACTTAA GGATTCGAGA AAGAGAACAT 150  
20 CTTTGTGTTAA AGAAGAGAAT AAGATTTTGG AAGAAAAAGT AATAGCAAAT 200  
TTGAAGAAGA AACAAGTTAC GTAGGGACGA GAACAAGTAA ATAAGGCCTA 250  
25 TCATGCATAT CGAGAGGTTT ACATTGATAG AGATAATTG AAGAGCAAAT 300  
GGACA 305

(2) INFORMATION FOR SEQ ID :1092:

- 30 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 237 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :1092:

40 AAATGGAAGT TGAAGTGAAGT GTGGTTTCCA GTACAGGGCA TCTGGCCACC 50

555

TTCACCTCAG TAAATACTGC TGATCGACTC TCTCTGGCTC TGGCTGTCCT 100  
GCCAGAGACA GCCAAACACA GGAGACATGA CAAATTACTA TCATCTTTTG 150  
5 CTTCTTTATT TTTATTATTA TTATTTTCT TTTTGTGGAG AACAGCGTCT 200  
TGCTGTATTG CCCAGCCTGA TCTCAAACCTC CTGGGCG 237

(2) INFORMATION FOR SEQ ID :1093:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 420 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

15

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :1093:

20

AGAAATTTAT TGCCTCACAG TTCTGGAGCC TGGAAGTGCA ATATCAAGGT 50  
GGAGACAGGG TTGGTTTCCT CTGGAGGCCA TAATGAAAGC ATCTGTTCCA 100  
25 GGTCTCTGTC CTTGGCTTGT AGAAACACGC ATTCTTCTGG TGGATCCACA 150  
CAGTCTTCTC CATGTGTATC CTCCTTCAG TTTCCCTTAT AGGACACCAG 200  
TGATGTCAGA TTAGGGATCG AACCCAACAA CCTCATTGTA AGTTACTCAC 250  
30 CTGTTTGAAA ACCCTATGTC CAAATACAGT TATAGTGTA GGAAGTAGGA 300  
CTTAGGGCTT ACAAATATGG AGTGGGGCAT CATCCAGACC ATACCATTTA 350  
35 AATTGCAGGG TTTCTCTCCA ATGTGAGTTA CATAACACA TTAAGGTTTG 400  
TGGGATTGAG AAAGGTATAC 420

(2) INFORMATION FOR SEQ ID :1094:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 192 base pairs

556

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :1094:

5	TTTTCTTGGG TAACCTCCCC TCCTTAATCC TTCTGGCATA GGCAGACTCA	50
10	CAGCAGGTAC CCAGTAGAAG GTAAGGTGGC TGATCATTTT TCCATAGGAG	100
	GTCTCCATGG CACACAGGGT AGAAAGTGCA TTCTGTGAAT TAGAGGCAGC	150
15	AGAGCATGGC AGCTAATGGA AACTGGCTCT GGGAGGTCAA AT	192

(2) INFORMATION FOR SEQ ID :1095:

(i) SEQUENCE CHARACTERISTICS:

20	(A) LENGTH: 228 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :1095:

30	AGAGAGCTTA ATAAGACCTA ACTACAGGCA AACCTGACTG GAACGTGAGT	50
	ATCTGTGGTC TGGTGTGGAA ATAGCTCTCT AGCCCCATCT CCCTCCTCCC	100
	ATTGTCCACC CCCATCCTCC TTACCACGAA ACACATTTTT CACCAGCATT	150
35	GCCAAACCAC TTGGGATTCC TGCGCATGGC TTTGCTTAGT TTGCTCTTCT	200
	GCTTCTTGGA TACCTCCTTC AGGAAATC	228

(2) INFORMATION FOR SEQ ID :1096:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 198 base pairs

557

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :1096:

ATTTTTTATG GAAAAGGGG GATAATGCAA AATAGCAAAA ATTGTAAACA 50  
10 AAGTTAAAGA TTATCTTCAT CTAAACCTTA AGCTGACAAT TTA AACACC 100  
TTGTGCATAA TGCAGAAAAA AACTGTCCGT TTGACTTCAC TTTCATTAC 150  
15 ACTGCTCCCT ACGCATGAGA AAGACCAGAT GTCTGGTTTC AGAGTATT 198

(2) INFORMATION FOR SEQ ID :1097:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 118 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :1097:

TAGAGAGAAG TTGATATATG AAGATAGGGT GGACAGGACT GTGAAGGAGG 50  
30 CTGAAGAAAA ACTGACTGAA GTGTCACAGT TTTTCTCTAC AAAACTGTGA 100  
CACTTCAGTC AGTTTTTC 118

35 (2) INFORMATION FOR SEQ ID :1098:

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 138 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1098:

5 AAAACTGACT AAAGTCANTG TGTAATACGA AAACCGAACA CTCCAGCAGT 50  
CCTATTTTAT NTNTTCCAAC CTAGNNCACC CAGGTGACGC NNGGGACTCG 100  
TCNCAGGTGT TTNGNACTTG CCGCCCGACN GGCNAAGG 138

## 10 (2) INFORMATION FOR SEQ ID :1099:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 151 base pairs  
(B) TYPE: nucleic acid  
15 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## 20 (xi) SEQUENCE DESCRIPTION: SEQ ID :1099:

ACTCCACCAC TGGNCCGCC ATGTTTTGGG TNGGNGCAAT GCGCTGTCTG 50  
TGAGCGCCAN TCTAATTGTA TTNGGACTGC ACGGGTCCGT AACTGACTG 100  
25 AACTGGGCT ACCTCGCCCG AAAATGNGAA CACCGCTCAA TATCGNTGCG 150  
G 151

## 30 (2) INFORMATION FOR SEQ ID :1100:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 201 base pairs  
(B) TYPE: nucleic acid  
35 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## 40 (xi) SEQUENCE DESCRIPTION: SEQ ID :1100:

TAGCAATAGG CTATAACATA AGCCGAGGTA TAGGCTACAC TAGCTAGGTT 50

559

CGTGTAAGTA CACTCTATAT TGGCACAACA TAAAATTAAC TAGTGACGCA 100  
TTTCTCAGAA TGCATCCCCA TCGTTAAGTG ACACAGACTG TCCCTCATAT 150  
5 CACCGGAGGA CTGGNCCAGG ACCTCCTGGC GGCACCAAAA TCCACGAGCG 200  
C 201

## (2) INFORMATION FOR SEQ ID :1101:

10

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 212 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 15 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1101:

20

TAGCAATAGG CTATAACATA TACCGAGGTA TAGGCTACAC TAGCTAGGTT 50  
CGTGTAAGTA CACTCTATAT TAGCACAACG ATAAAATTAA CTAGTGATGC 100  
25 ATTTTTCAGA ATGCATCCCC ATCGTTAAGT GACACATGAC TGTCCCTCAG 150  
TATCACTGGA GGA CTGGGNC CAGGACCTGA CCTGGTGGTA CAAAATCCA 200  
TGAGGCNGNA AT 212

30

## (2) INFORMATION FOR SEQ ID :1102:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 218 base pairs
- 35 (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1102:

560

CGGTAGCAAT AGCTATAACA TATAGCCGAG GTATAGGCTA CACTAGCTAG 50  
GTTTCGTGTAA GCACACTCTA TACNNGCACA ACATAAAATN AACTAGTGAT 100  
5 GCATTTCTCA GAATGCATCC CCATCGTNAA GNGACACATG ACTGTCCCTC 150  
AGTATTACTG NAGGACTGGN CCAGGACCTC CCTGGGGTAC CAAAATCCAN 200  
GAGTGGAAAT TCCANCAT 218

10

(2) INFORMATION FOR SEQ ID :1103:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 207 base pairs  
15 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :1103:

GTAGCAATAG GCTATAACAT ATACCGAGGT ATAGGCTACA CTAGCTAGGT 50  
25 TCGTGTAAGT ACACTCTATA TTAGCACAAC GATAAAATTA ACTAGTGATG 100  
CATTTTTTCAG AATGCATCCC CATCGTTAAG TGACACATGA CTGTCCCTCA 150  
GTATCACTGG AGGACTGGGN CCAGGACCTG ACCTGGTGGT ACCAAAATCC 200  
30 ATGAGCG 207

(2) INFORMATION FOR SEQ ID :1104:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 259 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
40 (D) TOPOLOGY: linear

561

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1104:

GGCGTCAAGT GGCCCAATCT AACAGCTCCA GGGTAGCCAC AACCATCGTG 50  
5 ATGGATTGCC ATTATTGTGT GCTAGTGGCT AGAGGTAGAC CCAATAGAAC 100  
TCTGCCCCAA CAGGGCAACA GCCAAGCTCA ATTCTCCAAG CCCCTGAAC 150  
AGACCTTCCA CATCCAGGAG AAGCTGTTGT TGTCTAGAGC TACTTAGTGT 200  
10 CAGAATCCAG GCCAGCTTGG CTGCTTGATG CGACTGGCTA TAGGATTNGN 250  
GTGNAGGCC 259

## 15 (2) INFORMATION FOR SEQ ID :1105:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 230 base pairs  
(B) TYPE: nucleic acid  
20 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## 25 (xi) SEQUENCE DESCRIPTION: SEQ ID :1105:

ACATGACCCC TTGGACTGAA GCGCTCAGT AGTAAAGGAG TGTCATGCAG 50  
GTCAACACAT GTCGCACATG GACCACAAAG CCTGCCACCA GCAGGATGCA 100  
30 CGGGGACTTC TGGGAGGGGG TGGACAGGAT ACTTATCTGT GACTGGAATG 150  
CAGGCGAGAG GCGGAGAAGA GAGTGAAGGA TAACTCATAG AGGGGGCAGC 200  
35 ATTTGTTTCG NGTTGAAAGA GGCAGAAAAT 230

## (2) INFORMATION FOR SEQ ID :1106:

## (i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 163 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double

562

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :1106:

ACATGNCCTG GACTGAAGGT GCTCAGTTAG TAAGGGAGTG TCATGCAGGT 50  
CAACACACGT CGCACATGGA CCACAAATGC CTGCCACCAC AGGATGCACA 100  
10 GGACTTTTGG GGGGAGTGGA CAGGTATTAT TGNGACTGGT GAGGTGAGAG 150  
GTNAGAGGGG GCT 163

15 (2) INFORMATION FOR SEQ ID :1107:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 182 base pairs  
(B) TYPE: nucleic acid  
20 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :1107:

ACNTGATGAT TGCCATTATT GTGTGCTAGT GGCTAGAGGT AGACCCAATA 50  
GAACTCTGCC CCAACAGGGC AACAGCCAAG CTCAATTCTC CAAGCCCCCT 100  
30 GAACAGACCT TCCACATCCA GGAGAAGCTG TTGTTGTCTA GAGCTACTTA 150  
GTGTCAAATC CAGGCCAGCT TGGCTGCTTG AT 182

35 (2) INFORMATION FOR SEQ ID :1108:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 214 base pairs  
(B) TYPE: nucleic acid  
40 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

563

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1108:

5           CCCCTGGACT GAAGGCGCTC AGTAGTAAAG AGTGTTCATGC AGGTCAACAC           50  
          ATGTGCGACA TGGACCACAA AGCCTGCCAC CAGCAGGATG CACGGGGACT           100  
          TCTGGGAGGG GAGTGGACAG GATACTATCT GTGACTGGAA TGCAGGCGAG           150  
10           AGGCGGAGAA GAGAGTGAAG GATAACTCAT AGAGGGGGCA GCATTTGTTT           200  
          CGNGCCTTGA AAGA   214

## (2) INFORMATION FOR SEQ ID :1109:

15

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 base pairs  
          (B) TYPE: nucleic acid  
          (C) STRANDEDNESS: double  
20           (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1109:

25

          ACATGGCCCC TGGACTGAAG GTGCTCAGTT AGTAAGGGAG TGTCATGCAG           50  
          GTCAACACAC GTCGCACATG GACCACAAAT GCCTGCCACC AGCAGGATGC           100  
30           ACAGGACTTT TGGGGGGGGT GGACAGGTAT TAT                               133

## (2) INFORMATION FOR SEQ ID :1110:

## (i) SEQUENCE CHARACTERISTICS:

- 35           (A) LENGTH: 156 base pairs  
          (B) TYPE: nucleic acid  
          (C) STRANDEDNESS: double  
          (D) TOPOLOGY: linear

40

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1110:

564

GCATGACCCC ATGGCACTGA AGGTGCTCAG GTTAGTAAGG GAGTGTCATG 50  
CAGGTCAACA CATGTCGCAC ATGGACCACA AATGCCTGCC ACCAGCAGGA 100  
5 TGCACGGGGG ACTTCTGGGA GGAGAGTGCA TAGGATACTT GTCTGTGACT 150  
GGAATG 156

## (2) INFORMATION FOR SEQ ID :1111:

10

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 282 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
15 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1111:

20

GGCGCTCANT GGATCCAATA CACCAGACTC CCGGGAGCGA AAACGCCCCG 50  
AGGTGCCTCA AAGAACTTAA AACAGAACTG CCATTAGACC CCACAATCTC 100  
25 ATNAAGGATG TTATAGATAT ATCCAAAAGA AAATAAATCA TTCTTCAAAA 150  
AGACACATAC ACTAACACGT TCATGGAGCA CTATTCACAC AGCAAAGACT 200  
CGATCAACTC ACACACTCAT GAATGCGGAT CGAAATAGAA GATGTGGTAT 250  
30 GCATACACCA CGAAATACTA CGAGCCATAA AA 282

## (2) INFORMATION FOR SEQ ID :1112:

35

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 181 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
40 (D) TOPOLOGY: linear

565

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1112:

TAATTAGTTT AACCACTGTG GAAAGCGTTG TAGGGTCTCA AAGACTNAAA 50  
5 ACAGAACTGC TTAGACCCCA CAATNTTANG AGCGGATGTT ATGATATATT 100  
CAAAAGGAAA TAAANNGNCN TGTNAAAGAC CATACACNAT NGTCCATCGG 150  
AGCCCGTATN CACGCAGCTT GTCATAACTA T 181

10

## (2) INFORMATION FOR SEQ ID :1113:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 278 base pairs  
15 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1113:

ATCCAATGAC ACCAGACTCC CGGGAGCGAA ACGCCCGCAG GTGCTCAAAG 50  
25 AACTTAAAC AGAACTGCCA TTAGACCCCA CAATCTCATN AAGGATGTTA 100  
TAGATATATC CAAAAGAAAA TAAATCATTC TTCAAAAAGA CACATACACT 150  
AACACGTTCA TGGAGCACTA TTCACACAGC AAAGACTCGA TCAACTCACA 200  
30 CACTCATGAA TGC GGATCGA AATAGAAGAT GTGGTATGCA TACACCACGA 250  
AATACTACGA GCCATAAAAG GCGAAATC 278

35

## (2) INFORMATION FOR SEQ ID :1114:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 125 base pairs  
(B) TYPE: nucleic acid  
40 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

566

(xi) SEQUENCE DESCRIPTION: SEQ ID :1114:

5 ACCTGCAAAC TTTTCTGTA AAGACCAGAT AGTAAGTATT TTATGCTTTG 50  
TGAGCCATAC AGTTTTTGTT GCAACTAGTC AACTCTCAAC TNACGTGGAC 100  
AGCATGTAAA GAACGAGAGT GACTG 125

10 (2) INFORMATION FOR SEQ ID :1115:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 157 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID :1115:

GTAGCGACCG GCGCTCATGG AATTCCGGGA CCTGCAAAC TTTTGAAAG 50  
ACCAGATAGT AAGTATTTTA TGCTTTGTGA GCCATACAGT TTTGTGCAA 100  
25 CTAGTCAACT CTCAACTCAC CGTGGACAGC ATGTAAATGG ATGGGAGTGG 150  
CTGCCGG 157

30 (2) INFORMATION FOR SEQ ID :1116:

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 123 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID :1116:

CCTGCAAAC TTTTCTGTAA AGACCAGATA GTAAGTATTT TATGCTTTGT 50

567

GAGCCATACA GTTTTTGTG CAACTAGTCA ACTCTCAACT NACGTGGACA 100

GCATGTAAAG AACGAGAGTG ACT 123

5 (2) INFORMATION FOR SEQ ID :1117:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 125 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :1117:

ACCTGCAAAC TTTTTTTGTA AAGACCAGAT AGTAAGTATT TTATGCTTTG 50

20 TGAGCCATAC AGTTTTTGTG CAACTAGTCA ACTCTCAACT CACCGTGGAC 100

AGCATGTAAA TGGATGGGAG TGGCT 125

(2) INFORMATION FOR SEQ ID :1118:

25 (i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 125 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :1118:

35 ACCTGCAAAC TTTTCTGTA AAGGACCAGA TAGTAAGTAT TTTATGCTTT 50

GTGAGCCATA CAGTTTTCGT TGCAACTAGT CAACTCTCAA CTCACCGTG 100

GACAGCATGT AAATGGATGG GAGTG 125

40

(2) INFORMATION FOR SEQ ID :1119:

568

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 148 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1119:

ATTAAGCTTG ACACATCTGT GTTATCACGC ACTGAAGACA GGAAGCAGTT 50  
CACTGAGTCA GCTGGCTTCC AAGCTTACAC AGAAGGCGAT AAGTCACTAT 100  
CAAAGAGCCA ATGAGAATCT TCTTATAGAA TAACCTGGGC CCAAGTGA 148

## (2) INFORMATION FOR SEQ ID :1120:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 240 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1120:

AGAATAACAG AGCCAAAGGA CTAATAAAAT CAATGAATCN TGGTGAGACT 50  
AATCAAGAAA AAATAGCACC AACAACAATG AGGAGAAAAT GGAAAAAGGG 100  
CAGAGTATTT CAAGATTAC GAGAGGGCAA ACCAATCAAC GAATGATTCT 150  
TAAGCCTTCA GTTTGCCCTG TAAGCAAACCT GAAGACGTGC AAGTCATCCT 200  
TTGCCCTGGG AGAGTTAACT TAACCCACAG GGACAACTAG 240

## (2) INFORMATION FOR SEQ ID :1121:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 254 base pairs

569

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :1121:

AAATGGGGAG AATCAACAGA GCCAAAGGAC TAATAAAATT AAGAATCCTG	50
GTGAGACTAA TAAGAAAAAA TACACCAACA ACAATCCGAG AAAATGGAAA	100
AAGGGCAGAG TATTTAATGA TACGAAGATG GGCAAACCAA TCAATGAATG	150
ATTTTAAAGC CTTACGTCT GCCCTGTAAG CAACTGAAG ACGTGCAAGT	200
CATCCTTCGG CCCTGGAGAG TTAACGTTNC CCAAGGGGCA ATGAGAAGGG	250
ACAG	254

20

(2) INFORMATION FOR SEQ ID :1122:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 253 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :1122:

AAACGAGGGG AGAATCAACA GAGCCAAAGG ACTAATAAAA TCAATGAATC	50
NTGGTGAGAC TAATCAAGAA AAAATAGCAC CAACAACAAT GAGGAGAAAA	100
TGGAAAAAGG GCAGAGTATT TCAATGATTA CGGAGAGGGC AAACCAATCA	150
ACGAATGATT CTTAAGCCTT CACGTTTGCC CTGTAAGCAA ACTGAAGACG	200
TGCAAGTCAT CCTTTGCCCT GGGAGAGTTA ACTTAACCCA CAGGGACAAC	250

40

570

GAG

253

(2) INFORMATION FOR SEQ ID :1123:

5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 210 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :1123:

15

AAATGGGGAG AATCAACAGA GCCAAAGGAC TAATAAAATT AATGAATCCT

50

GGTGAGACTA ATAAGAAAAA ATACACCAAC AACAATCCGA GAAAATGGAA

100

AAAGGGCAGA GTATTTAATG ATACGAAGAT GGGCAAACCA ATCAATGAAT

150

20

GATTTTTAAG CCTTCACGTC TGCCCTGTAA GCAAACCTGAA GACGTGCAAG

200

TCATCCTTTG

210

25

(2) INFORMATION FOR SEQ ID :1124:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 231 base pairs

(B) TYPE: nucleic acid

30

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :1124:

AAATGGGGGG AGAATCAACA GAGCCAAAGG ACTAATAAAA TTAATGAATC

50

CTGGTGAGAC TAATCAAGAA AAAATAGCAC CAACAACAAT CAAGAGAAAA

100

40

TGGAAAAAGG GCAGAGTATT TAAATGATTA CGGAGACGGG CAAACCAATC

150

571

AACGAATGAT TCTTAAGCCT TCATGTTTGC CCTGTAAGCA AACTGAAGAC 200

GTGCAAGTCA TCCTTTGGAC CCTGGGAGAG T 231

5

(2) INFORMATION FOR SEQ ID :1125:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 89 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :1125:

AAGTCCCATC AGCAACCCGT TTTTACCAG ATGTCACTCA AGAATGCGCC 50

20 CGTGGCCCTC CAGTTCCTGC GCACTAAGAG CGTCCCGCT 89

(2) INFORMATION FOR SEQ ID :1126:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 205 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :1126:

AAGAAACCCG AGACMCCAAC TAATCCCAGA ACAGCTAAAA CCAATAAAGA 50

35

ACCAAAACTT CACGACCACT TTCCTGAGGA CCCTGCTGAG TGCTCATGAC 100

ACCAATACTG ACAATTGTAG CGGTAATACA TACAATGATT TAATAAGCCT 150

40

ATGCTACTGG ACACATGCCC ACACAATAAT ANTCANRTGT NTYGTTAGGC 200

CTACT 205

572

## (2) INFORMATION FOR SEQ ID :1127:

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 151 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1127:

GCAAGGCCTG GCCGACAACA CCCTTATTGC-TAAAGTAAAT AATGNCGCGC 50  
15 GGGGCCTGGA CCACCCTCTG GAAGAAGATT GTACCTTGGA GCTTCTCAAG 100  
TCTGAGGATG AGGAAGCTCA GGCAGTGTAT TGGCGCTTTA GTATCACATA 150  
A 151

20

## (2) INFORMATION FOR SEQ ID :1128:

## (i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 237 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1128:

GAGCACCCCA GCCCATAACA CAGAACTCGT CCCCCTACCC CCCTCAGCAA 50  
35 GCCGGAGAGG CTAGCCCAAG TAATCATAAY AACAGCCGCC CGAGAGCAGC 100  
CCCAGTAGCA GCCCCATGGC CGGGCGGAAC ACCTACATCG ACAACCTCAT 150  
GACAGACGAG ACCTGCCAGG ACGCAGCCAT TGCGGGCTGC AAGGCCTCRC 200  
40 CCTTCGTCTG GGCCGCCGTC CCCGGAGAAA CGCTCGT 237

573

## (2) INFORMATION FOR SEQ ID :1129:

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 126 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1129:

GCCTCGTGGA AGTGACATAG CCTTTAAACC CTGCGTGGCA ATCCCTGACG 50  
15 CACCACGTGA CGCCCAGGAA AGACAGGGCG ACCTGGAAGT CCAACTACTT 100  
CCTTAAGATC ATCCAACATAT AGGATG 126

## (2) INFORMATION FOR SEQ ID :1130:

20

## (i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 246 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1130:

GCCATCTTCT GTAACAAAAT AAATAGTGTC AAGCACTAAA TATATGCATG 50  
AATGCATCAG CAATAAGATG ACAATCAAAG AATGCTGTGA AGATTGGCAT 100  
35 CAAGATGTTA GCAGCATACT GCAGGACTAG GCTTAGAAGC CTACCTGCAG 150  
TTTATTTGCA AGGATTTTTT TTTTCGRGGGC GGAGGGGAGA GAAAAGTAAA 200  
TGTGCTAACT TCGGATACTT GCCCTTATAA AGAATTCCTT YGTATC 246

40

## (2) INFORMATION FOR SEQ ID :1131:

574

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1131:

10 CGAGGATCCG GGTACCATGG CAAGTCTCAT GAGGCTATTT ACCGAATTTA 50  
 TCCTCTGTCT GACCATGATT TTTTCCCTCA AATACAACCA CTCCTCGACT 100  
 15 TTTCACCCTC AAAGTATAAA AAGTATGAAA NATAAACAAG CTCTTGCACT 150  
 GTACACTTAG AAGTGTACAA TTAAAGCATT ATAGAGCTAT CTACACACCG 200  
 ATAAATCCCA TCGAATCTTG AATAATCCAT CAATACGTAG AACGCAAGGG 250  
 20 TGCAGACAGA ACTAAAACCA ACT 273

## (2) INFORMATION FOR SEQ ID :1132:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 329 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1132:

35 GAGGATCCGG GTACCATGGT CTGTATATCT GTGCTTCCAC TTCTCGGAGG 50  
 TGGTAGAGGG GAGGCTGTCC TCTGGTCAGG AGAATCCTAT TCAGTGCTCC 100  
 CTTAGACATT CTTCCAGGCA GGATCAAACCT CAAAGGAAAA GGAATTTGTG 150  
 40 AAGCAAACCA TGGCTTTGTC ACAGTAAAGT AATTGTCACT CTCACCCAG 200

575

AATGTGTGAA GCGCTGCAGG GAGAAGCTTC TCTTCCAGGA GAGCAATANA 250

AGCCAATGTA TCTGACCCTT GCTTYGATGA GAGTTAATAA TAAGTATTAT 300

5 ATTTCTGTTT GTTAAAAAGT TCAGAATTT 329

(2) INFORMATION FOR SEQ ID :1133:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 24 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :1133:

CCCCGAGCTA GTTGTCCCGA CCTG 24

20

(2) INFORMATION FOR SEQ ID :1134:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 297 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :1134:

GAGGATCCAC AAACCATGGA ACACTCTCGC GGCTGCCACT CCCCCATGAC 50

35 CACCCTACAG GCCCTAACCC CAGCCCCTCA CGTTATCGTC CAGCCACAAA 100

TAGCTGCCGC CCTGAGATCT CCACCTCAGA CCCTCTCCCG AAGCCCACAG 150

CGGCCCCCTGC CGGGCACCCC AGCTTCCTCG CAGGCACCAA AAGCGCAGTT 200

40

CCAGGAATCT CTACCCTAGA GTGATCCGGC GCCAGTTGCC AGTTAAGGGA 250

576

CCAAACCTCG CCAGAAGGCT TCTTTTCGGG TTGATCGCCA TCTATTY

297

(2) INFORMATION FOR SEQ ID :1135:

5 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 93 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :1135:

15 GCCGCTTTAC TGCTCAGTTC GGAGCTACCG CTTCGAAAGC AACAAAAAAG 50

CNTTTGCAAA TGAAACGAGA TTGCTGAATT GCGTACACCG AGA 93

(2) INFORMATION FOR SEQ ID :1136:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 334 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

25

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :1136:

30

CGAGGATCCG GGTACCATGG AGCTTCACAC GGGTCTTCTT GGTCTCAGGG 50

TTGTGGGAGA TAACGGTGGC ATAGTTCCTT GATGCCCGGG CCAGCTTGCC 100

35 ACGGTCTCCA GGCTTCTCCT CCAGGCAGCA CACGATTGTA CCCTCAGGCA 150

TGGTGCCAC AGGGAGCACA TTGCCAATGT TGAGCTGGGC CTTCTTGCCG 200

CAATACACAA ACTGGCCCGT GNGAATGCCC TCGCGGGCAA TGAACAGTTC 250

40

CGCCCGCTTC TTAAACCAAG ACAGATCCCC GAAGGCCGCC TGGGCAAGGG 300

577

GCCCCCTCRAA CCCGGGGCTA TACACGTCAA AATC

334

## (2) INFORMATION FOR SEQ ID :1137:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 199 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1137:

15 CGAGGATCCG CATACCATGG CCCCCATCTT ACGAGCCCTT ACTCCTCATG 50  
ATGAAGAAAC TCCAAACCCT TTGACAGCTC CTCGGGGTNA AACCTGGNAY 100  
AAAGCTGACT GACCAGGCTC CATGAAATCT CCCATCTCCA TRATGTACCT 150  
20 CCTTGRTGCC ATCTCTATAT AAAGMGAACC AGTCCTAAAA TCAAACACT 199

## (2) INFORMATION FOR SEQ ID :1138:

- 25 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 304 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1138:

35 CGAGGATCCA AATACCATGG CGCTCCCTCC TCCCGAGCGC CGCTCCGCGT 50  
GGCACCCGGC TCGCTCCGAG TTTCAGGCTC GTGCTAAGCT AGCGCCGTCG 100  
TCGTCTCCCT TCAGTCGCCA TCATGATTAT CTACCGGGAC CTCATCAGCC 150  
40 ACGATGAGAT GTTCTCCAAC ATCTACAAGA TCCGGGAGAT CGCGGACGGG 200

578

TTGTGCCTGG AGGTGAAGGG GAAGATGATC ACTAGGACAG AAGGTAACAT 250

TGMTGACTTG CTCATTGGTG GAAATGCTTC CTCTGAAGGC CCCGAGGAAG 300

5 AAGG 304

(2) INFORMATION FOR SEQ ID :1139:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 277 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :1139:

GAGGATCCGG GTACCATGAG AAACCTTTGAA GCCAGAGATT TTAAACAATC 50

20 AAGGCACTTG AAAACATTAA GTATATGTAC AAATGTGCAA GTAAAACAAA 100

CAGCTGTACC AACGAGTAAC AAAGAAACAG TAAATCTTCA TCTTAACAAC 150

25 CTTTAATAGT TATCTAAATG CAGAGTTTGT TTATGAAATG AACCAAAGCA 200

GTTTGTCATT TCTTACTATA AAATACCGAA AATAAAGTGC AAAACTTAGC 250

30 CACTACTGGC TAAAGAACT AAGTAAA 277

(2) INFORMATION FOR SEQ ID :1140:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 208 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :1140:

579

CGAGATCCGG GTACCATGGC CTCCTACAGG TGCCGTGGAG CCACGCCCAA 50  
AAGAGAGCTC CCTGAGAAAC TCGTTGATGC CTTGCTCACT GAAGGAGCCT 100  
5 TTTAGCAGAG CAAATTTTCAT CTTGCGTGCA TTGATGGCGG CCATGGCGGG 150  
GTACCCAAAC CCTCCAATTC CCAACGCGGT CTCAAGTTCA GACTGGGCTC 200  
CAGCTTCT 208

10

(2) INFORMATION FOR SEQ ID :1141:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 274 base pairs  
15 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :1141:

CGAGGATCCG AGTACCATGG CCTCGAACTG AGCATCAATA TATTCTACTG 50  
25 CCAGCTTATA ACTGTCATCT TTATTCATAT GGTCTCCAAA TCCCACGATG 100  
TCAACAATGG TTAACCTCAG CCGTACATTG CTTTCCTGAA GCTCATAACT 150  
TCTGGCTTTT AACCGAACAC CTGGTTCATT GTGAGTAGCT GGGTCACTTT 200  
30 TAAATTTGGT GTTGAACAAA GTGTCCATTA ACGTGGATTT GCCAATGCCT 250  
GTCTCACCAA TACAAAGGAT GTTG 274

35

(2) INFORMATION FOR SEQ ID :1142:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 226 base pairs  
40 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

580

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1142:

5 GCCTGCACAT TGACTGTGGG AAAC TCGGAA ACAAGCTCAC ATCTCCCCGT 50  
GGGAAACCTT CTAGCAACAG GATGAGTCTG CAGTGAAGT CAGTTGCCAC 100  
CTTCCTCTAT GCGGAGGTCT TTGTTGTGTT GCTTCTCTGC ATTCCCTTCA 150  
10 TTTCTCCTAA AAGATGGCAG AAGATTTTAA AGTCCCGGCT GATGGAGTTG 200  
TTAGTGCCT ATGGTAACAC CTTCTT 226

## (2) INFORMATION FOR SEQ ID :1143:

15

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 168 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
20 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1143:

25

RGGRTCCRNG TGCCRTGGGG YNTNNCTAGR CRGCRGGYAA GGTCCACCRC 50  
TGRRCRGNTG NCNGTGAGGR CRTGNRGGNC CRTGCGAGTG GGCTTACCGN 100  
30 TAGGTTCGGG AATGACCTTG CYMACGNCNN YGACAGCTAA GTRGRNGCRG 150  
GNANGRTGNN GTGGAGRG 168

## (2) INFORMATION FOR SEQ ID :1144:

35

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 256 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
40 (D) TOPOLOGY: linear

581

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1144:

CGAGGATCCA AATACCATGG AGCTGACAAT GTCAGCTCAA TTTGAAGTAT 50  
5 TCTTGAGGGA CCTTTTGCTC ATAGGCTTTA ATTCTGTCTG TGACTTTTGC 100  
CAGGATTTGA GGAAATCGAC TGCCTTCACT CTTCCCTGAA ACTTTGAAGT 150  
CCACATAAGG GCTTTCTCAT CAAATGGCAG AAATTATAAT TTATAAACCT 200  
10 AAACAACCTT ATAGTGTTTT CGCTTTGAAT TGTATGAATT CTTAGAAGTG 250  
AGAAGT 256

## 15 (2) INFORMATION FOR SEQ ID :1145:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 184 base pairs  
(B) TYPE: nucleic acid  
20 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## 25 (xi) SEQUENCE DESCRIPTION: SEQ ID :1145:

AAACACAAGG CTAAAAGTCA CTAAAGGTGA CACAGTACCA ACCCCGGGAA 50  
GGTTGAGTTC TGTGCTGCTA CCTTCTACTG ATGGCGAATA GACTATTCTG 100  
30 TACCCTGTGA TGGGAGCCTG GGGTCTGCTC CAGCAAACAA CAATCGAGGT 150  
GTAATCAACT TGGTCCACAG TCGGGTCAGG AGGG 184

## 35 (2) INFORMATION FOR SEQ ID :1146:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 221 base pairs  
(B) TYPE: nucleic acid  
40 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1146:

5 CGAGGATCCG GGTACCATGG CCCAAAGAGT GAATGATGTA TCCCAGGGCG 50  
CAGTCCACAA CTTGCGCAGT ACCTTCCCAG ATGACAGCCT CACTGGACCG 100  
ATTTCCATCC ACGAAGATGA TGCTAAGAAG CACCATGAGC AGACCCAGCT 150  
10 TGGGTGAGTC CTTAGTCGTT CCCAGTATGC CTGCATCAGT GGGCTCTAAG 200  
GTGCTGAGAA GAATGCACAA G 221

## (2) INFORMATION FOR SEQ ID :1147:

15

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 255 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
20 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1147:

25

CGAGGATCCA AATACCATGG GAGTCAAGCA TGCCTCGATA GCCACAGATT 50  
TACAAGAATT ACCTACAGTT TGCTTCTTNG AATCGACATG CAAATCTGCT 100  
30 TAAGGATTCT CACATTCAGG ACAGAGAACA AATTTTTTAA TGAATCCATC 150  
CAACAGGTCT TGNAGTTTAT TCGCCTCATG AGATCCATTG ATAATGGAAC 200  
RRTMATTCTT AACANCAAAC NGMGMCTGNN NTCCCRNCTT ATAACCMAAA 250  
35 GATNT 255

## (2) INFORMATION FOR SEQ ID :1148:

40

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 230 base pairs  
(B) TYPE: nucleic acid

583

(C) STRANDEDNESS: double

(D) TOPOLOGY: lin ar

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :1148:

	CGAGGATCCA GGTACCATGG ACGATTACACA GCCCCTGGCC ACTGGCCATT	50
10	TCCAGTGGTA GGGAGCACAC TGRTACATT CGAGACCCAC CACGTTGAGC	100
	AGACAAAGGC AGCCTCCACT CTCCTCGTCA CTCAACATGT ACCTCCGTCC	150
	CCCAGGATGT TGTAGTTATA GCAATAGCAG CCCTGCGGTT GACGTAGGTG	200
15	AGTCGGTGAC GCCCGATTG GATCGGGTGT	230

(2) INFORMATION FOR SEQ ID :1149:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 223 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :1149:

30	GTGCCGTTGG TCCTGTGCGG TCACTTAACC AAGATGCCTG AGGAAACCCA	50
	GACCCAAGAC CAACCAATGG AGGAGGAGGA GGTGAGACG TTCTCCTTTC	100
	AGGCAGAAAT CGCCCAGTTG ATGTCATTGA TCATCAATAT TACCNACTAG	150
35	AACAAAGAGA TCTTTCTGAG AGAGCTTATT CAAAATACAT TAAATGTATT	200
	GGACAAAATT CGATATAAAA GCT	223

40

(2) INFORMATION FOR SEQ ID :1150:

(i) SEQUENCE CHARACTERISTICS:

584

- (A) LENGTH: 272 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1150:

10	CGAGGATCCG AGCACCATGG AGAGACTATG ACGCTCAACA AGAATCACTC	50
	GGAGGGCGAC GGAGTGATCG TCAATAACAC CGAGATATC CTAATGCCCT	100
	ATGATCACGT GGAAC TAACA TCAATGACA TGAAGAACGT GCCAGAAGCC	150
15	TTCAAAGAGA CCAAGAAAGG CGCTGTCTAC CTTACTTCTC ATTGAACCAT	200
	CTTTATGTCC AAGAACAAGG ATGCGATGGG TATTTCGTGA NGCTATTTGA	250
20	NMTRAGGRMA GNCTGNAAGG TM	272

## (2) INFORMATION FOR SEQ ID :1151:

## (i) SEQUENCE CHARACTERISTICS:

- |    |                            |
|----|----------------------------|
| 25 | (A) LENGTH: 140 base pairs |
|    | (B) TYPE: nucleic acid     |
|    | (C) STRANDEDNESS: double   |
|    | (D) TOPOLOGY: linear       |

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1151:

	TGAGGATTTA TAGATTANAG CTAGAGTTCA CATTTTATGG ATTACAACCA	50
35	AAAAAACCT GAAAAGAAA AAAACAAAA AAGCTCAAAA GCAATCACAA	100
	GGATAGTTGA ATCCCTCTTT AAACCCCCAA AGCAACCCCC	140

## (2) INFORMATION FOR SEQ ID :1152:

## (i) SEQUENCE CHARACTERISTICS:

585

- (A) LENGTH: 208 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1152:

10	AAGGATCCGG GTACCATGTA TTCCCCGGT ATCAGCAGAG GCGTGACGG	50
	GCACTGCTTT AAAACTGGGA AGGAGGAAGA CGAGGCCAGG GAGCCGGAGG	100
	GTCACCAAGG TAGATTTCCA GCAGCCTAGT CCAGCTGAAC GCTTTCAGC	150
15	CTTGCTTTTT AGCAGCTTTG AGGAAAAGTA TAGTGATCCG GATGTGAAAC	200
	TTTCATTG	208

## 20 (2) INFORMATION FOR SEQ ID :1153:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 274 base pairs
- (B) TYPE: nucleic acid
- 25 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## 30 (xi) SEQUENCE DESCRIPTION: SEQ ID :1153:

	CGAGGATCCA GGTACCATGG GGTGGATCCG CCGGGCATAG CCACCCTGGA	50
	TGGTGGCCAT GGTGAGGCCG ATGAGGAAAA ACATCTTCCC CTGCTGTAGG	100
35	CTACTGAACT GGAAGCGCTG GTGTGTGAGG AAGCTCAACG TGCACTCCAG	150
	GCCCAAGAAC AGGAAGAGGT AGAGGAAGTA GACTMGGCCC AGGCGGCCAG	200
40	GCTGATGAAT TGTCTCCAAA GGGTGAGACC TGGCCACGAG CCATANCCCA	250
	GAMGCCNMAC AGGGCTRGGG ACTG	274

586

## (2) INFORMATION FOR SEQ ID :1154:

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 267 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1154:

GAGGATCCAC CGACCATGGA ACACTCTCAA TGGCTGCAAC CACCCCGTGG 50  
15 CCCCCCTACC AGCCCCAATC TCCAAACCCC GCACGTCGAT CATGACGCCA 100  
CCAACAGCTG CAGCCCCCTGA GATCTTCACC TTAGACCCTC TCCCGAAGCC 150  
CGCAGCCGCC CCTGCGAACC CTCCAACCTG TTCACACGCG CCGAAAGCCT 200  
20 ATTCCCAGGA CTCTCTGCCC CTACGTGACC GNCCCTAGCT GCTAGTCGAG 250  
AATCCGAACT CCGCTCC 267

## 25 (2) INFORMATION FOR SEQ ID :1155:

## (i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 231 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1155:

CTCAAACCCC GNTTCCCCC TAATAAGAGC AACTAAAAA CTTCTGATAA 50  
CCACAATAAA AGCGTGCATT TGAGCACAAT TCAAAAGCCA ACCCCTTCGA 100  
40 AGGNGCTTCT GATGNAAAAG GAGTTATGTT GAACGAAGCA GGAGTTAACG 150

587

CTACACAGTC AAATTGTGGC ATTAGGACGC GCGAGCGGGC TAGCTGCGGC 200  
CGTCTANCAA GGCAACGGCC GCCTTTGAAT T 231

5 (2) INFORMATION FOR SEQ ID :1156:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 128 base pairs  
(B) TYPE: nucleic acid  
10 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :1156:

GCGCGAGCAC AGAGCCTCGC CTTTGCCGAT CCGCCGCCCA TCCACACCTG 50  
CCGCCAGCTC ACCGTGTATG ATGATATCAC CNCGCTCGCC ACCAACRACG 100  
20 GCTCYAACMT GTGCAAGGCC GCCTTCAA 128

(2) INFORMATION FOR SEQ ID :1157:

25 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 126 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :1157:

35 GCCGCAACAC AAGCCAGGGA GACTCAAGNC CACAGGGGCC CCCC GGCTCT 50  
GAGGGATTCA CCGTCGCCTC CCGGTCCCCG AAGGCCACACA AGGGCAGAAA 100  
GGTGAGCCTT ATGCACTGCC TAAAGA 126

40

(2) INFORMATION FOR SEQ ID :1158:

588

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 101 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1158:

AATAACCATA ACTGCAAAAA CCCAAMCAAA AAAAAAGGGG GAACAAAAAA 50

CCCCAAACCC CCAAAAAAAC CAGAAAAAAC CACAAAAAA AACCCTCCT 100

T 101

## (2) INFORMATION FOR SEQ ID :1159:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 172 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1159:

GAGGATCCGG GTACGGGCAG GGTGAGAGCC TGGGGTCCAC CGATAACCGG 50

GAGGGAGATG GCGTTCTTGA GCAGAGGGGA TGGGCCGTCC GGGAGCTCCC 100

CCCACACACG GTGGCGGTGC GGGTGAACTG GAAGGGGAGG TCGAAGGTGC 150

CATCTTCTTC AGGCCCTCC AC 172

## (2) INFORMATION FOR SEQ ID :1160:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 235 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

589

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :1160:

GAGGATCCAC ATACCATGGA ACAGCACCAC AAAAATAGCC ATTTTGATCA 50  
TGGTTATTTC CCAGGACCAC ACGATTGCG TACGTCCTG GAAGGCTATG 100  
10 TGTCTGTTCT GAGCCTTCCC ACTCTCCTAA AGGGCAGATG AAGATCAGAG 150  
CTTTGACCCT GTGATGCCAT TTTAATCAAC CCTGCTTGGT TTTAGAGGAT 200  
15 TGCTCCCGTG GGTCACTTGA GGCAGGCTCC ACCTT 235

(2) INFORMATION FOR SEQ ID :1161:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 284 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :1161:

GAGGATCCAC CAACCATAGA AAGTAAATAC TGTATAAAAA GCTCCAGCTG 50  
30 TTAGATACAA ATGCAAAACG CTCCTAAAA AACGGCCTGA AAAAAAATC 100  
ACAGACAATG CCAAACCTTA TAGGTCTGTA TTTTCCTTTA TACAAAATGC 150  
35 CCTCAAATTA AAAAGTAATT CCCATATAGC AATAAAGTCC ACATCTCTGG 200  
ATTACCTATA ACCGGTATTA TGGGGTGTGT TTATACTGCC TAGAATGTTA 250  
ACCCTCATAA AGCCTTAAAA GTACATTTGT GAAA 284

40

(2) INFORMATION FOR SEQ ID :1162:

590

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 287 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1162:

10

GCTCACATAA ATTTCTTCAC CGACCCTTTT CCTTCAGCT TCCTTACTAT 50

AAAAAACCCC ACA AATA TGTCATCAT CATCCATACT AACCAACCCC 100

15

GTCACCATCT CAATCAGCAG CAAGTCCTAC TCTCTGTGGG TGAAACCTTG 150

TTACCACCTC TAGGGGCAGA CCCCTTTTCA GATATATTCA AGAGTTTAAT 200

ATCCTCCCAC TATAGCGCTT CGACTTTGTA TCTTCCTCTA TGGCTACCAA 250

20

ATTCTGTCCG TTGATAAGTA CTGGCTCTAA ACCATGC 287

## (2) INFORMATION FOR SEQ ID :1163:

25

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 122 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1163:

GAGGATCCAA AAACCATAAA ATTCATCATC CCCAGCAGGT GCNCTAGCTA 50

TACTTTATTA CAGCAAARCA CAACCACACG CTGAMCTANM TCGTATAGAT 100

AAACACCAAT CATGGGTCGG CC 122

40

## (2) INFORMATION FOR SEQ ID :1164:

591

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 142 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1164:

10

GCGCGGGTCT GTCTCTTGCT TCAACAGTGT TTGGACGGAA CAGATCCGGG 50

GACTCTCTTC CAGCCTCCGA CCGCCCTCCG ATTNCTCTC CACTTGCAAC 100

15

CTCCAAGACC ATCTTCTCGG CCATCTCCTG CTTCTGAAGC CT 142

## (2) INFORMATION FOR SEQ ID :1165:

## (i) SEQUENCE CHARACTERISTICS:

20

(A) LENGTH: 219 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1165:

TATTCCCCCG GTATCAGCAG AGGCGTGTAC GGGCACTGCT TTAAACTGG 50

30

GAAGGAGGAA GACGAGGCCA GGGAGCCGGA GGGTCACCAA GGTAGATTTC 100

CAGCAGCCCT AGTCCAGCTG AACACTTTCC AGCCTTGCTT TTCAGCAGCT 150

35

TTGAGGAAAA GTATAGTGAT CCGTATGTGA AATTTTCATC GCACGTAGCG 200

GATGAGAATA GAGAACTCA 219

## (2) INFORMATION FOR SEQ ID :1166:

40

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 202 base pairs

592

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :1166:

10 GAGGATCCAC CAACCATAGA AAGGAAACAA CACTTGGAGT GAACCCGACC 50  
CAAGCCACTA CACCCCAGCC TAACCGACAG GTGCTAGACT AATNGTNAAA 100  
AACAAACCGGA AAATAGACCC GGACGAAGAT CAAAGNTTNT CAATCCAAAC 150  
15 ATTTTAGGGG GACCAAGACC CMGGGATCAA AAACAAGGTC CACCACACCC 200  
AA 202

(2) INFORMATION FOR SEQ ID :1167:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 159 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
25 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :1167:

30

GAGAAACCTA CCCAACCAAG AGGCGCCCTG CTTTGTAAATG ACCTTTACGA 50  
AGACACGTCT GATACCCAAC CTGACAGAGG AAACAACAGT AGTCTGAAAG 100  
35 GGACAGAATG AGAGAGGGGG CTGGAGAAAG AAATGAATAA ACATGAATGC 150  
ATCTGGAGA 159

(2) INFORMATION FOR SEQ ID :1168:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 211 base pairs

593

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :1168:

CCCTAGACAA GCCACCTGAG GAGAGGCTCG GAGCCGGGCC CGGACCCCGG	50
CGATTGCCAC CGCTTCTCTC TAGTCTCACG AGGGGTTTCC CGCCTCGCAC	100
CCCCACCTCT GGA CTG CCT TTCCTTCTCT TCTCCGCGTG TGGAGGGAGC	150
CAGCGCTTAG GTCGGAGCGA GCCTGGGGCC ACCGCCGTGA AGACATCGCG	200
GGGACCGATT C	211

20

(2) INFORMATION FOR SEQ ID :1169:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 211 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :1169:

30

GGATTTCCGG TCCTGGCTTT CTGATATTTT TAAAATCGAC CTGGAATCAA	50
CCATTGACAT GTCCTGTGCT AAATATGAAT TCACTGATGC CCTGCTGTGC	100
CATGATGATG AGCTGGAAGG GCGCCGGATT GCCTTCATCC TGTACCTGGT	150
TCCTCCCTGG GACAGGAGCA TGGGTGGTAC CCTGGACCTG TACAGCATTG	200
ATGAACACTT T	211

40

(2) INFORMATION FOR SEQ ID :1170:

594

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 266 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1170:

10 GAGGATCCGC GCAACCATAG AACTCACAAC CCAGCCATAT ACCTCAGACA 50  
CAATGGAATG GCGGGAGGTC GAGGTNGACA AACCTGAGT AATGTTGGGC 100  
15 ACTTCCGCAC CGGAGCTGTT CTTACCTTTG ATAAAGTGA TGTTATTGCT 150  
ATTAATGATC TCTTAACGGA CTTCAACTGT AAAATTNGCA TGATCTAGTC 200  
CTATCCACCA ACGNCGAACA ATATGCTGTT GCCAMGATTG AGCACGAGCC 250  
20 GTTTGGGCTC AACGGC 266

## (2) INFORMATION FOR SEQ ID :1171:

## 25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 167 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
30 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1171:

35 GGCACAACCC ACTTTGAACA ATCATGCTTC AGAAATCTGC CTGACCTTAG 50  
CTGCTGCTGC TGCTCACTTT ATTATAGTAT AACTTCGGTA GGCATACTTG 100  
GAGAACATAT CCCACATTAG GAATTGATTT AAGCCTGAGA GTTTGAGGGC 150  
40 TTTAATCCTT TAAAACT 167

595

## (2) INFORMATION FOR SEQ ID :1172:

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 232 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1172:

AATAAACCTC CCTATCACAG TGACCTACTA CCCGCGTGTG CTTATATAAC 50  
15 TAATCCAGGA CAACCCACAA AAATTATAGC AACACACAAA CACACCGCTG 100  
ACCATAACAT GTGCGTCTTT CAAAGATGCC TTATCAACCA GAGCGATGAT 150  
TACTGAGGAT ACGCAACTCA TAAACTCTA CTAAAGCAA CAGGGCAGAC 200  
20 GTGCGTCTGT GCCAGTCGTG AATGTGGTGA AC 232

## (2) INFORMATION FOR SEQ ID :1173:

25

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1173:

35 GAGGATCCAC CAACCATAGC CCGAAAATGT GGTAAGGGAC CCTCATCTAT 50  
CACACAACNC AGGTAAGAAG GCACCCAGCC CCATGGGCCA TAC 93

## (2) INFORMATION FOR SEQ ID :1174:

40

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 200 base pairs

596

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :1174:

GCCTTTTTTT ACCCGCCGGA AGCTACAGCT TTTGCCCCCC CAAAAAACC 50  
10 CCACCCTTTT ACCCACC GCG GACCCAAAAA CAGCAAAAAC CAAGGACCTC 100  
TCCCAACCCC AACCCCTCCT TTTTGGCCCT TCCTTCCCCC CCTCCCAGCC 150  
15 CACCCCCAGA CACCTCAATC CCCCAAAGG ATGCCCTAAA CCTCTCCTAA 200

(2) INFORMATION FOR SEQ ID :1175:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 121 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :1175:

GAGGATCCAA AAACCATGGC ATTCATCAGC CCCAGCAGGT GTCCCAGCCA 50  
30 TGACTIONACCA TAGCAAAACA CAACCACACA CTAACCTGCA TCGCCTAGCT 100  
TACTGATGAT GATGTCCTGG T 121

35 (2) INFORMATION FOR SEQ ID :1176:

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 26 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :1176:

AACCAGACAC GCCGACCCGC TGAATC

26

5

(2) INFORMATION FOR SEQ ID :1177:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 178 base pairs

10

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :1177:

GAATCGATCT TGACCTGGCT GCCAGGAATA TCCAGCTTGT TACCGACTGG

50

20

TAAAGAATAA GACCGCTGAT CATAGAGTGA AGCTCCAGGA ATCAGAGAGT

100

CTCATAGCAA ACCTCGAAAC TGAGGATGAG ATGGTTACAG ATAAAGCCTT

150

TCAGGATGGA TTMAAGNAMG CAGAGAGG

178

25

(2) INFORMATION FOR SEQ ID :1178:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 144 base pairs

30

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :1178:

GGTTAAGTTT TTCATCAAAG ACTCAGGTAC CTATTATCGT TCCCTGGCGA

50

40

AACTGAGGAG AAAAGTTAAT CAACCAGGTT ACTCCACAG TTTGCCCGTG

100

TGTTATGCAT CAGTTATACA GGTATCCAC CAAGTTCAAG TCAA

144

598

## (2) INFORMATION FOR SEQ ID :1179:

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 233 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1179:

GACCAGGGAG GAGGTTTAAT CAACTTGGAC CCCCTCCGGC CTAGCCGCCG 50  
15 AGGAGGTGCA TTCGGGACAA CCACTAGGTC AGAACGCAGC CTCTCCAGAG 100  
TCCTCAGGCT CGACAACGAT TATCCTGCTG CTATCAGCT TTGATTTACT 150  
GATCTCGCTG AAAAGACAGA CGCTTTTAGA TACCGAGTCG ATAGGGGGTC 200  
20 TCGCGTACTT TTCAGTAGAT AGGTGGTGCT TGT 233

## (2) INFORMATION FOR SEQ ID :1180:

25

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 225 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1180:

35 CGAGGATCCG GGTACCATGG GCCGGATACA ACGAGCTATC ATTACTGCTC 50  
CCATGGCCAA AACCAGCAGT CCCACAATCC CCGTGAAAGG GATGAGGTAA 100  
TAGCCCAAGG GGAAGGTATT GTCTGGAACC AGAAGCGCCC GAGCCCCCTT 150  
40 CTTGTAGRCA AAGAGGGCGC CCAGGTGCTT GGAGCTNCTN TCCCCAATGG 200

599

AGGTAGACGG GACCAAGATC TGCTG

225

## (2) INFORMATION FOR SEQ ID :1181:

5

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 293 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1181:

15

TGAGGATTTA AAAATTCTGG AATATCTATG ATTGATCGTC AACTTTATTC

50

GATGAATAAG CTTGATGTGG CCTAGTTTTN NGNNNNNTGG NYATGGTNNA

100

TCNNNTTANT TTTTGGTTG TTGTGNATAT TATNGAATAR AMGAATRGNG

150

20

TTTAGAGTTT GGAAGCGGCN RNCGTARMG NNACTCYACG CTCGCNNCTN

200

TTGNNNNACA GMRGGNTCTC TNGGRTGAGT GGRTNCMGTT GGMGGNNTCN

250

25

NNNTAGCTGN NGNGAGRATC AGCTRGCTTN CTTTGNNGCTN GCT

293

## (2) INFORMATION FOR SEQ ID :1182:

30

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 252 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

35

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1182:

GAGGATCCGG GTACCATGGC TCTCTCTTTC TTTTTTTTCT TTTTCTTGCC

50

40

GGATGTGAGA GCTGCCTGAG ATTCAAGGTC ATCCGGCAGC TCAGTCCCCA

100

600

CCACCTCTGT CTCTGGCTCC ACTGTGGCAT CTTGCTGTTT TTCTTTCTCA 150  
GTCTTCTCTT AGGGAGCTGC CAGAGCTGCC TGGACCTGAG AATTCATTCC 200  
5 TTCTGGCTGT TGAGACCCCG TGGACTCCCC TGGATTCCAG AGNNTNATTT 250  
NG 252

## (2) INFORMATION FOR SEQ ID :1183:

10

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 202 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
15 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1183:

20

ACGAGGATCT GAATACTCTG GCCTGCAAGT AGAGGCTAAT TCGATGTGTG 50  
AAACTGTAGA TTCGGCTTAA GGTAATAGTC ATTTATAGAC TATTCAATAG 100  
25 AGTCAGACTG GTCGAGGCTG GTAAGTGTAG CGGAACGGTT GCTGACTGAT 150  
ATTGTTAGAG TGAGGCTTGT ACTGGTGTGT ATCCGTAGGT GGTCTGCAGT 200  
GT 202

30

## (2) INFORMATION FOR SEQ ID :1184:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 base pairs  
35 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1184:

601

CAGATCCTCA GCTTTCGTGG TTCACAATTT CTCAGTCTC TTA

43

(2) INFORMATION FOR SEQ ID :1185:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 48 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :1185:

15 ACCGTCCTTC TGGTTCATCC TAGCAAAAAT CTCACCATCT TCTATCAC

48

(2) INFORMATION FOR SEQ ID :1186:

- 20 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 104 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :1186:

30 ACATCATCCG AGTCCCCTCT ACAGTGTTC TGTGATCGT TGCATCCCCC

50

TGGTTTGGAA ATAAATATA AACTGCCCCG CAAGAGATAA AATTGTATTT

100

TTTA

104

35 (2) INFORMATION FOR SEQ ID :1187:

- 40 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 76 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

602

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1187:

5 CTGGTTCTGT TTCTCGCAGG TGGTAGAGGG GAGGCTGTCC TCTGGTCAGG 50  
AGAATCCTAT TCAGTGCTCC CTTAGA 76

## (2) INFORMATION FOR SEQ ID :1188:

10 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 42 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear  
15

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1188:

20 AATAGGGCGC GATCAACTCT TAACTTTGAG GAGAACCAAC AA 42

## (2) INFORMATION FOR SEQ ID :1189:

(i) SEQUENCE CHARACTERISTICS:  
25 (A) LENGTH: 253 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear  
30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1189:

GGCGGACGTG CGCGCCTTGT CTTGCGGCA CCTGGGCCTG AGGTGCGTGC 50  
35 CTCCCGGGCC CTCGCCAGCT CCAGATGCGT GAGGAGGACT TCAGAAACCC 100  
GACTGAGAAG TGGAGCAACC CCCAGGAAGG GCCGGACCTG CCTAAATGCC 150  
40 GCCAAGGCCT TTTATTTATG GCTAGTTTGC TCTCGTGAAA TACTAACATC 200  
GTTTTAATGG CACTCATCAA GTACGCAAAT GATATGATTT AACCTCGCGC 250

603

AAT

253

## (2) INFORMATION FOR SEQ ID :1190:

5

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 252 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1190:

15

GAGGATCCAC CAACCATAGA ACGGCCCTAC TAATGAACCA CACAAGCTAG

50

TTGCACCACT ATAGAAACAC AAAACTACAC ATCTATACCA ATAAAAATAA

100

CAACTACTCC AATTGCCCAT GTGGTATTGT CGCAGACTGA AATGAATTAT

150

20

GAATTTAGGT TGATTACCAA TATCGGCATA AAATAAACTR TGTAAAGGCTC

200

AMTATGTTGA CAGTAAGCTC TTGTCAGGTG TCTAATGAGG TAAAAGCATT

250

25

TT

252

## (2) INFORMATION FOR SEQ ID :1191:

30

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 178 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

35

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1191:

GAGGATCCAA CAACCATAGA GCACATAAAA ACCGCCCAAC GATCTAACTA

50

40

ATATACAACG GCTAACCGGG CCATTCAAAA GCTCGCCCAG ATTAAATGCC

100

604

TGCCGANAGC AAGTACATGG GGAGGATTAC TACTTCCTGG TTGCCAACCA 150

CCCTTCCGGC TGCCCTTG TGACTTG 178

5 (2) INFORMATION FOR SEQ ID :1192:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 156 base pairs  
(B) TYPE: nucleic acid  
10 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :1192:

GGATCGGCGG TAATCGGTGA GCTCGGTGTC GGGTAAGGGA CCCAGTCCAT 50

CGCCACCAAG CGCCAGGAAT GGGCAGCATA AGGGAAGGCT AAGGAGGACT 100

20 GCAACAGGTT AGGGCCCTGG AGATTGTATT TAGCAAGGGT ACCTGCGNNG 150

NGGGCA 156

25 (2) INFORMATION FOR SEQ ID :1193:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 99 base pairs  
(B) TYPE: nucleic acid  
30 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :1193:

ATTCTGAATC TTTAATGAAA ATCAGCCCAG AGCTTGTTGT AATACAGACA 50

TAAGTGAAG AGCATGCCCA CAGCTTAGAG AGGTTGTACC AAATTTAGA 99

40

605

## (2) INFORMATION FOR SEQ ID NO: 1194

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

5

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID : 1194:

NNNNTCCTTC TCCTGCGACA GACA

24

15

## (2) INFORMATION FOR SEQ ID NO: 1195

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

20

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID : 1195:

TGTCTGTTCG AGGAGAAGGA

20

30

## (2) INFORMATION FOR SEQ ID NO: 1196

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

35

40

## (xi) SEQUENCE DESCRIPTION: SEQ ID : 1196:

AANNTCTCGG ACAGTGCTCC GAGAAC

26

606

## (2) INFORMATION FOR SEQ ID NO: 1197

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 26 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID : 1197:

TTNNTCTCGG ACAGTGCTCC GAGAAC

26

15

## (2) INFORMATION FOR SEQ ID NO: 1198

## (i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 22 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID : 1198:

GTTCTCGGAG CACTGTCCGA GA

22

30

## (2) INFORMATION FOR SEQ ID NO: 1199

## (i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 23 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

40

## (xi) SEQUENCE DESCRIPTION: SEQ ID : 1199:

GTTCTCGGAG CACTGTCCGA GAG

23

607

## (2) INFORMATION FOR SEQ ID NO: 1200

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 23 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID : 1200:

GTTCTCGGAG CACTGTCCGA GAC

23

15

## (2) INFORMATION FOR SEQ ID NO: 1201

## (i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 22 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID : 1201:

CTGTCTGTCTG CAGGAGAAGG AA

22

30

## (2) INFORMATION FOR SEQ ID NO: 1202

## (i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 22 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

40

## (xi) SEQUENCE DESCRIPTION: SEQ ID : 1202:

CTGTCTGTCTG CAGGAGAAGG AG

22

608

## (2) INFORMATION FOR SEQ ID NO: 1203

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID : 1203:

AGCTCGGCTC GAGTCTG

17

15

## (2) INFORMATION FOR SEQ ID NO: 1204

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

20

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID : 1204:

GCGACAGACA GCAGACTCGA GCCG

24

30

## (2) INFORMATION FOR SEQ ID NO: 1205

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

35

40

## (xi) SEQUENCE DESCRIPTION: SEQ ID : 1205:

GATCCGGCTC GAGT

14

609

## (2) INFORMATION FOR SEQ ID NO: 1206

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

5

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID : 1206:

CCGAGAACAC TCGAGCCG

18

15

## (2) INFORMATION FOR SEQ ID NO: 1207

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

20

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID : 1207:

GTAAAACGAC GGCCAGT

17

30

## (2) INFORMATION FOR SEQ ID NO: 1208

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

35

40

## (xi) SEQUENCE DESCRIPTION: SEQ ID : 1208:

CGAGGTCGAC GGTATCG

17

610

## (2) INFORMATION FOR SEQ ID NO: 1209

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 17 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID : 1209:

CGAGGTCGAC GGTATCG

17

15

## (2) INFORMATION FOR SEQ ID NO: 1210

## (i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 56 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID : 1210:

TACGTTTCGAC AAGCTTGAAT TCGCGGCCGC TTTTTTTTTT TTTTTTTTTT

50

TTTTTT

56

30

## (2) INFORMATION FOR SEQ ID NO: 1211

## (i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 11 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

40

## (xi) SEQUENCE DESCRIPTION: SEQ ID : 1211:

611

GCCWSCGCCG A

11

(2) INFORMATION FOR SEQ ID NO: 1212

- 5 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 24 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID : 1212:

15 GGTGGCGACG ACTCCTGGAG CCCG

24

(2) INFORMATION FOR SEQ ID NO: 1213

- 20 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 24 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID : 1213:

30 TTGACACCAG ACCAACTGGT AATG

24

35 In the above SEQUENCE LISTINGS, some sequences are preferred because they fall into the category of sequences referred to hereinbefore which exhibit no more than 90% homology to a human sequence known per se. The preferred sequences in these terms are all of sequences SEQ ID Nos 1 to 1193, EXCEPT FOR SEQ ID Nos:

40 85, 117, 177, 197, 223, 248, 317, 354, 355, 483, 829, 1057, 594, 595, 597, 164, 427, 420, 58, 67, 374, 373, 501, 569, 188, 550, 904, 932, 97, 89, 134, 433, 434, 357, 4, 6, 11, 336, 529, 544, 545, 549, 1037, 847,

612

870, 871, 872, 873, 875, 876, 579, 199, 524, 544, 513, 380, 276, 291,  
615, 623, 627, 634, 635, 648, 652, 617, 619, 684, 697, 718, 720, 1127,  
1145, 1148, 1164, 938, 587, 589, 588, 241, 243, 335, 61.

5

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15

## CLAIMS:

1. A nucleic acid fragment encoding a gene product or portion thereof and comprising any one of:-
  - (a) a sequence selected from SEQ ID Nos 1 to 1193;
  - (b) an allelic variation of a sequence as defined in (a); or
  - (c) a sequence complementary to (a) or (b).
2. A nucleic acid sequence as set out in any one of SEQ ID Nos 1 to 1193, or a complement or allelic variation thereof.
3. A sequence as claimed in claim 2 and which exhibits no more than 90% homology to a human sequence known per se.
4. A nucleic acid fragment comprising a portion of a sequence as defined in claim 2 or claim 3 of sufficient size such that a probe of the same size and exhibiting complementarity to said portion can hybridize to said sequence as defined in claim 2 or claim 3.
5. A fragment as claimed in claim 4, wherein said portion is at least 15 bases in length.
6. A fragment as claimed in any one of claims 1, 4 or 5 and encoding at least a portion of a biologically active polypeptide.
7. A nucleic acid sequence as claimed in claim 2 or claim 3 and encoding at least a portion of a biologically active polypeptide.
8. A DNA construct comprising a fragment as defined in any one of claims 1, 4, 5 or 6 or a sequence as defined in any one of claims 2, 3 or 7, together with a control or regulatory sequence.
9. A construct as claimed in claim 8 which encodes a fusion protein comprising a known protein and the polypeptide encoded by said fragment or sequence.
10. A construct as claimed in claim 9, wherein the fusion protein encoded is a cleavable fusion protein having an endopeptidase recognition site positioned between codons corresponding to said known

614

protein and said fragment or sequence.

11. The use of a fragment as defined in any one of claims 1, 4, 5 or 6 or a sequence as defined in any one of claims 2, 3 or 7 to produce a gene.

12. A DNA fragment comprising a gene obtainable by the use defined in claim 11.

13. An expression vector comprising a fragment as defined in any one of claims 1, 3, 5 or 6, a sequence as defined in any one of claims 2, 3 or 7, a DNA construct as defined in any one of claims 8 to 10, or a DNA fragment as claimed in claim 12, positioned such that that nucleic acid sequence which encodes the polypeptide corresponding to said fragment, sequence or DNA fragment is in operable reading frame with a control or regulatory sequence.

14. A vector as claimed in claim 13, wherein said vector control or regulatory sequence comprises a regulatable promoter.

15. Host cells which incorporate as a heterologous part of their expressible genetic information a fragment as defined in any one of claims 1, 3, 5 or 6, a sequence as defined in any one of claims 2, 3 or 7, or a DNA fragment as defined in claim 12.

16. A process for the production of a polypeptide comprising cultivating host cells as defined in claim 15.

17. An antibody directed against a polypeptide obtainable by the performance of a process as defined in claim 16.

18. An antibody as claimed in claim 17 and which is monoclonal.

19. A novel gene product or portion thereof encoded by a fragment as defined in any one of claims 1, 3, 5 or 6, or encoded by a sequence as defined in any one of claims 2, 3 or 7, or encoded by the gene comprised in a DNA fragment as defined in claim 12.

40



## INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

<b>(51) International Patent Classification 5 :</b> <b>C12N 15/11, 15/62</b> <b>C12P 21/08, C07K 15/28</b> <b>C12Q 1/68</b>	<b>A3</b>	<b>(11) International Publication Number:</b> <b>WO 94/01548</b> <b>(43) International Publication Date:</b> 20 January 1994 (20.01.94)
<b>(21) International Application Number:</b> PCT/GB93/01467 <b>(22) International Filing Date:</b> 13 July 1993 (13.07.93) <b>(30) Priority data:</b> 9214857.6 13 July 1992 (13.07.92) GB <b>(71) Applicant (for all designated States except US):</b> MEDICAL RESEARCH COUNCIL [GB/GB]; 20 Park Crescent, London W1N 4AL (GB). <b>(72) Inventors; and</b> <b>(75) Inventors/Applicants (for US only) :</b> SIBSON, David, Ross [GB/GB]; 37 Grimsdells Lane, Amersham, Buckinghamshire HP6 6HF (GB). GROSS, Jacqueline [GB/GB]; 47 Boxmoor Road, Kenton, Middlesex HA3 8LH (GB). HADFIELD, Kathryn, Mary [GB/GB]; 5 Carlisle Terrace, St Ives, Huntingdon, Cambridgeshire PE17 4PQ (GB). HOWELLS, David [GB/GB]; 77 Puttocks Drive, Welham Green, Hatfield, Hertfordshire AL9 7LW (GB). STARKEY, Michael [GB/GB]; 27 Creasy Close, Abbots Langley, Hertfordshire WO5 0HS (GB). KELLY, Maria [IE/GB]; 24A Oxford Road, Ealing, London W5 3ST (GB). SHAW, Diana [GB/CA]; 342 Glacier Hall, University of Calgary, 2500 University Drive NW, Calgary, Alberta T2N 1N4 (CA).		<b>(74) Agent:</b> BIZLEY, Richard, Edward; Hepworth Lawrence Bryer & Bizley, 2nd Floor Gate House South, West Gate, Harlow, Essex CM20 1JN (GB). <b>(81) Designated States:</b> AT, AU, BB, BG, BR, BY, CA, CH, CZ, DE, DK, ES, FI, GB, HU, JP, KP, KR, KZ, LK, LU, MG, MN, MW, NL, NO, NZ, PL, PT, RO, RU, SD, SE, SK, UA, US, VN, European patent (AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG). <b>Published</b> <i>With international search report.</i> <i>Before the expiration of the time limit for amending the claims and to be republished in the event of the receipt of amendments.</i> <b>(88) Date of publication of the international search report:</b> 31 March 1994 (31.03.94)
<b>(54) Title:</b> HUMAN NUCLEIC ACID FRAGMENTS, ISOLATED FROM BRAIN ADRENAL TISSUE, PLACENTA OR BONE MARROW  <b>(57) Abstract</b>  This invention provides a nucleic acid fragment encoding a gene product or portion thereof and comprising any one of: (a) a sequence selected from SEQ ID Nos 1 to 1193 from the attached sequence listings; (b) an allelic variation of a sequence as defined in (a); or (c) a sequence complementary to (a) or (b). The invention includes uses of such fragments, and gene products corresponding thereto.		

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CA	Canada	KP	Democratic People's Republic of Korea	RU	Russian Federation
CF	Central African Republic	KR	Republic of Korea	SD	Sudan
CG	Congo	KZ	Kazakhstan	SE	Sweden
CH	Switzerland	LI	Liechtenstein	SI	Slovenia
CI	Côte d'Ivoire	LK	Sri Lanka	SK	Slovak Republic
CM	Cameroon	LU	Luxembourg	SN	Senegal
CN	China	LV	Latvia	TD	Chad
CS	Czechoslovakia	MC	Monaco	TG	Togo
CZ	Czech Republic	MG	Madagascar	UA	Ukraine
DE	Germany	ML	Mali	US	United States of America
DK	Denmark	MN	Mongolia	UZ	Uzbekistan
ES	Spain			VN	Viet Nam
FI	Finland				

## INTERNATIONAL SEARCH REPORT

International Application No.

PCT/GB 93/01467

<b>I. CLASSIFICATION OF SUBJECT MATTER</b> (If several classification symbols apply, indicate all) <sup>6</sup>		
According to International Patent Classification (IPC) or to both National Classification and IPC:		
Int.Cl.5	C 12 N 15/11	C 12 N 15/62
C 07 K 15/28	C 12 Q 1/68	C 12 P 21/08
<b>II. FIELDS SEARCHED</b>		
Minimum Documentation Searched <sup>7</sup>		
Classification System	Classification Symbols	
Int.Cl.5	C 12 N	C 12 Q
		C 07 K
Documentation Searched other than Minimum Documentation to the Extent that such Documents are Included in the Fields Searched <sup>8</sup>		
<b>III. DOCUMENTS CONSIDERED TO BE RELEVANT<sup>9</sup></b>		
Category <sup>10</sup>	Citation of Document, <sup>11</sup> with indication, where appropriate, of the relevant passages <sup>12</sup>	Relevant to Claim No. <sup>13</sup>
Y	SCIENCE vol. 252, 21 June 1991, LANCASTER, PA US pages 1651 - 1656 ADAMS, M. ET AL. 'Complementary DNA sequencing: expressed sequence tags and human genome project' see the whole document ---	1-19
Y	PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF USA vol. 88, March 1991, WASHINGTON US pages 1943 - 1947 PATANJALI, S. ET AL. 'Construction of a uniform-abundance (normalized) cDNA library' cited in the application see the whole document --- -/-	1-19
<p><sup>10</sup> Special categories of cited documents:</p> <p>"A" document defining the general state of the art which is not considered to be of particular relevance</p> <p>"E" earlier document but published on or after the international filing date</p> <p>"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)</p> <p>"O" document referring to an oral disclosure, use, exhibition or other means</p> <p>"P" document published prior to the international filing date but later than the priority date claimed</p> <p>"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention</p> <p>"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step</p> <p>"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.</p> <p>"&amp;" document member of the same patent family</p>		
<b>IV. CERTIFICATION</b>		
Date of the Actual Completion of the International Search	Date of Mailing of this International Search Report	
08-10-1993	01. 03 94	
International Searching Authority	Signature of Authorized Officer	
EUROPEAN PATENT OFFICE	ANDRES S.M.	

## III. DOCUMENTS CONSIDERED TO BE RELEVANT (CONTINUED FROM THE SECOND SHEET)

Category	Citation of Document, with indication, where appropriate, of the relevant passages	Relevant to Claim No.
Y	NUCLEIC ACIDS RESEARCH vol. 18, no. 19, 11 October 1990, ARLINGTON, VIRGINIA US pages 5705 - 5711 KO, M.S.H. 'An 'equalized cDNA library' by the reassociation of short double-stranded cDNAs' cited in the application see the whole document ---	1-19
Y	NATURE vol. 355, 13 February 1992, LONDON GB pages 632 - 634 ADAMS, M. ET AL. 'Sequence identification of 2,375 human brain genes' see the whole document ---	1-19
Y	GENE vol. 81, 1989, AMSTERDAM NL pages 295 - 306 AKOWITZ, A. & MANUELIDIS, L. 'A novel cDNA/PCR strategy for efficient cloning of small amounts of undefined RNA' see the whole document ---	1-19
P,Y	WO,A,9302214 (MEDICAL RESEARCH COUNCIL) 4 February 1993 see the whole document -----	1-19

# INTERNATIONAL SEARCH REPORT

national application No.  
PCT/GB93/01467

## Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This international search report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:  
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☐ Claims Nos.:  
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:
3. ☐ Claims Nos.:  
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

## Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see PCT/ISA/206 mailed on 29.11.93

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

1-19(all partially)

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.  
☐ No protest accompanied the payment of additional search fees.

GB 9301467  
SA 76316

**The European Patent Office is in no way liable for these particulars which are merely given for the purpose of information.**

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
WO-A- 9302214	04-02-93	None	